

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 17:12:40 ; Search time 183 Seconds
(without alignments)
170.693 Million cell updates/sec

Title: US-10-719-623A-16

Perfect score: 306

Sequence: 1 MFTLKSLLLFLGTLINLS.....EVEKRFPPVIGRLINGILGK 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	306	100.0	61	1	TEMG_RANTE
2	245	80.1	61	1	TEMH_RANTE
3	219.5	71.7	58	1	RLXN_RANCA
4	212	69.3	66	1	RLXN_RANCA
5	211.5	69.1	71	1	BRIE_RANES
6	189.5	61.9	65	1	GGNS_RANRU
7	184.5	60.3	69	1	BR1B_RANPI
8	155	50.7	331	2	Q7T2V5
9	148	48.4	80	1	GGN4_RANRU
10	145	47.4	71	1	RN2P_RANPI
11	144	47.1	62	1	PLR_RANPI
12	138.5	45.3	74	1	BR7A_RANTE
13	138.5	45.3	74	1	BR7B_RANTE
14	137.5	44.9	74	1	BR2F_RANES
15	136	44.4	62	1	RAYT_RANTE
16	135	44.1	70	1	RN2A_RANPI
17	133	43.5	66	2	Q800R3
18	120	39.2	84	1	ES1B_RANES
19	116.5	38.1	62	2	Q800F1
20	111	36.3	71	2	Q800S2
21	110	35.9	75	2	Q800R8
22	109	35.6	72	1	GALE_KASSE
23	109	35.6	77	1	DRG3_PHYBI
24	108	35.3	75	2	Q800R9
25	107	35.0	75	2	Q800S0
26	106.5	34.8	72	1	DM55_AGAAN
27	106	34.6	81	1	DRG1_PHYBI
28	106	34.6	201	1	DEM_PACDA
29	105.5	34.5	76	1	DMS4_PHYBI
30	105	34.3	72	1	DMS4_AGAAN
31	105	34.3	79	2	Q7T3K6

32	105	34.3	79	2	Q7T3K7
33	105	34.3	80	1	DMS2_PACDA
34	103.5	33.8	70	2	Q800R4
35	103.5	33.8	73	1	DMS2_AGAAN
36	103.5	33.8	76	2	Q7T3K8
37	103	33.7	71	2	Q800S1
38	103	33.7	75	1	DMS2_PACDA
39	103	33.7	77	1	DRG2_PHYBI
40	103	33.7	78	1	DMS1_PHYBI
41	103	33.7	80	1	DMS6_AGAAN
42	103	33.7	81	1	DMS2_PHYBI
43	102.5	33.5	72	1	DMS6_PHYBI
44	102.5	33.5	77	1	DERB_PHYBI
45	101.5	33.2	72	2	Q800R6

Q7c3k7 phyllomedus
Q93453 pachymedusa
Q800r4 phyllomedus
Q93222 agalychnis
Q7c3k8 phyllomedus
Q800s1 agalychnis
Q93452 pachymedusa
Q902k5 phyllomedus
P80282 phyllomedus
Q93226 agalychnis
P31107 phyllomedus
P81490 phyllomedus
Q9pt75 phyllomedus
Q800r6 litoria cae

ALIGNMENTS

RESULT 1

ID	TEMG_RANTE	STANDARD;	PRT;	61 AA.
AC	P79875;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Temporin G precursor.			
OS	Rana temporaria (European common frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.			
OX	NCBI_TaxID=8407;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RA	MEDLINE=97175050; PubMed=9022710;			
RA	Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,			
RA	Barra D.;			
RT	"Temporins, antimicrobial peptides from the European red frog Rana			
RT	temporaria.";			
RL	Eur. J. Biochem. 242:788-792(1996).			
CC	-!- FUNCTION: Has antibacterial activity against Gram-negative and			
CC	Gram-positive bacteria.			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- TISSUE SPECIFICITY: Skin.			
CC	-!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.			
CC	Brevinin subfamily.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; Y09395; CAA70564.1; -			
DR	InterPro; IPR004275; Brevinin.			
DR	Pfam; PF03032; Brevinin; 1.			
KW	Amidation; Amphibian defense peptide; Antibiotic; Signal.			
FT	SIGNAL 1 22 Potential.			
FT	PROPEP 23 44			
FT	PEPTIDE 47 59 Temporin G.			
FT	MOD_RES 59 59 Leucine amide (G-60 provides amide			
FT	group).			
SQ	SEQUENCE 61 AA; 7171 MW; EDF5A8BC79DFD9F2 CRC64;			

Query Match 100.0%; Score 306; DB 1; Length 61;

Best Local Similarity 100.0%; Pred. No. 3.8e-25;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFTLKSLLLFLGTLINLSLCEERDADEERDDLEERDVEVEKRFPPVIGRLINGILG 60

DB 1 MFTLKSLLLFLGTLINLSLCEERDADEERDDLEERDVEVEKRFPPVIGRLINGILG 60

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QY      61 K 61
DB      61 K 61

RESULT 2
TEMB_RANTE
ID      TEMB_RANTE      STANDARD;      PRT;      61 AA.
AC      P79874;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Temporin B precursor.
OS      Rana temporaria (European common frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX      NCBI_TaxID=8407;
RN      [1]
SEQUENCE FROM N.A., SEQUENCE OF 47-59, AND SYNTHESIS OF 47-59.
RC      TISSUE=Skin, and Skin secretion;
RX      MEDLINE=97175050; PubMed=9022710;
RA      Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA      Barra D.;
RT      "Temporins, antimicrobial peptides from the European red frog Rana
RL      temporaria.";
RL      Eur. J. Biochem. 242:788-792(1996).
CC      -!- FUNCTION: Has no antibacterial activity.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- TISSUE SPECIFICITY: Skin.
CC      -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC      Brevinin subfamily.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; Y09394; CAA70563.1; -
CC      InterPro; IPR004275; Brevinin.
CC      Pfam; PF03032; Brevinin; 1.
DR      Anidation; Amphibian defense peptide; Direct protein sequencing;
KW      Signal.
FT      SIGNAL      1      22      Potential.
FT      PROPEP      23      44      Temporin H.
FT      PEPTIDE      47      56      Leucine amide (G-57 provides amide
FT      MOD_RES      56      56      group).
FT      SEQUENCE      58 AA; 6806 MW; 684ACB0451E5E81 CRC64;
SQ      -----
Query Match      71.7%; Score 219.5; DB 1; Length 58;
Best Local Similarity 73.8%; Pred. No. 5.8e-16;
Matches 45; Conservative 7; Mismatches 6; Indels 3; Gaps 1;

QY      1 MFTLKSLLLFLGTLINSLCEERDADDERDLEERDVEVEKFFPVGIRLNGILG 60
DB      |||||
DB      1 MFTLKSLLLFLGTLINSLCEERDADDERDLEERDVEVEKFFPVGIRLNGILG 60
QY      61 K 61
DB      58 K 58

RESULT 4
RLXN_RANCA
ID      RLXN_RANCA      STANDARD;      PRT;      66 AA.
AC      F39084;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Ranalexin precursor.
OS      Rana catesbeiana (Bull frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX      NCBI_TaxID=8400;
RN      [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 47-66.
RC      TISSUE=Skin, and Skin secretion;
RX      MEDLINE=94193792; PubMed=8144672;
RA      Clark D.P., Durell S., Maloy W.L., Zaoloff M.;
RA      "Ranalexin. A novel antimicrobial peptide from bullfrog (Rana
RT      catesbeiana) skin, structurally related to the bacterial antibiotic,
```

RT polmyxin.";
 RL J. Biol. Chem. 269:10849-10855 (1994).
 RN [2]
 RP STRUCTURE BY NMR OF RANALEXIN.
 RX MEDLINE=98237592; PubMed=9578480;
 RA Aumelas A.; Chavanieu A., Roch P., Chiche L., Grassy G., Calas B.,
 RA "Solution structure of the antimicrobial peptide ranalexin and a study
 RT of its interaction with perdeuterated dodecylphosphocholine
 RT micelles.";
 RL Eur. J. Biochem. 253:221-228 (1998).
 CC -!- FUNCTION: Potent microbicidal activity, active against S.aureus
 CC and E.coli. It acts as well as a membrane-disruptive agent at
 CC higher concentrations.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- DEVELOPMENTAL STAGE: Expression starts at metamorphosis and
 CC continues into adulthood.
 CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
 CC Brevinin subfamily.
 CC
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 CC -----
 DR EMBL; S69903; AAB30394.1; -;
 DR PIR; A53744; A53744.
 DR InterPro; IPR004275; Brevinin.
 DR Pfam; PF03032; Brevinin; 1.
 KW Amphibian defense peptide; Antibiotic; Direct protein sequencing;
 KW Hemolysis; Signal.
 FT SIGNAL 1 20 Potential.
 FT PROPEP 21 44 Small acidic peptide.
 FT PEPTIDE 47 66 Ranalexin.
 FT DISULFID 60 66
 SQ SEQUENCE 66 AA; 7615 MW; 096B8AD59A3C8513 CRC64;
 Query Match 69.3%; Score 212; DB 1; Length 66;
 Best Local Similarity 72.9%; Pred. No. 4.2e-15;
 Matches 43; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MFTLKSLLLPFLGTINISLCEERDADDEERDDLEERDVEVEKFFVIGRILNGIL 59
 Db MFTLKSLLLPFLGTINISLCEERDADDEERDDLEERDVEVEKFFVIGRILNGIL 59
 RESULT 5
 BR1E_RANES STANDARD; PRT; 71 AA.
 AC P32412;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Brevinin-1E precursor.
 OS Rana esculenta (Edible frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8401;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=94216303; PubMed=8163497;
 RA Simmaco M., Mignogna G., Barra D., Bossa F.;
 RT "Antimicrobial peptides from skin secretions of Rana esculenta.
 RT Molecular cloning of cDNAs encoding esculentin and brevinins and
 RT isolation of new active peptides.";
 RL J. Biol. Chem. 269:11956-11961 (1994).
 RN [2]
 RP SEQUENCE OF 48-71, AND DISULFIDE BOND.

RC TISSUE=Skin secretion;
 RX MEDLINE=93285327; PubMed=8508915; DOI=10.1016/0014-5793(93)81384-C;
 RA Simmaco M., Mignogna G., Barra D., Bossa F.;
 RT "Novel antimicrobial peptides from skin secretion of the European frog
 RT Rana esculenta.";
 RL FEBS Lett. 324:159-161 (1993).
 CC -!- FUNCTION: Shows antibacterial activity against representative
 CC Gram-negative and Gram-positive bacterial species, and a very high
 CC hemolytic activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
 CC Brevinin subfamily.
 CC
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 CC -----
 DR EMBL; X77831; CAA54842.1; -;
 DR PIR; C53578; C53578.
 DR InterPro; IPR004275; Brevinin.
 DR Pfam; PF03032; Brevinin; 1.
 KW Amphibian defense peptide; Antibiotic; Direct protein sequencing;
 KW Hemolysis; Signal.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 45
 FT PEPTIDE 48 71 Brevinin-1E.
 FT DISULFID 65 71
 FT VARIANT 60 60 L -> F (in brevinin-1E).
 SQ SEQUENCE 71 AA; 8267 MW; 10900AC2BC71BB73 CRC64;
 Query Match 69.1%; Score 211.5; DB 1; Length 71;
 Best Local Similarity 71.0%; Pred. No. 5.1e-15;
 Matches 44; Conservative 7; Mismatches 10; Indels 1; Gaps 1;
 QY 1 MFTLKSLLLPFLGTINISLCEERDADDEERDDLEERDVEVEKFFVIGRILNGIL 59
 Db MFTLKSLLLPFLGTINISLCEERDADDEERDDLEERDVEVEKFFVIGRILNGIL 60
 QY 60 GK 61
 Db 61 PK 62
 RESULT 6
 GGN5_RANRU STANDARD; PRT; 65 AA.
 ID GGN5_RANRU
 AC P80399; Q91329;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Gaegurin-5 precursor.
 GN Name=GGN5;
 OS Rana rugosa (Wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Park J.M., Lee J.Y., Moon H.M., Lee B.J.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 42-65.
 RC TISSUE=Skin secretion;
 RX MEDLINE=95091844; PubMed=7999137;
 RA Park J.M., Jung J.-E., Lee B.J.;
 RT "Antimicrobial peptides from the skin of a Korean frog, Rana rugosa.";
 RL Biochem. Biophys. Res. Commun. 205:948-954 (1994).


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Query Match          48.4%; Score 148; DB 1; Length 80;
Best Local Similarity 49.3%; Pred. No. 3.3e-08;
Matches .34; Conservative 11; Mismatches 14; Indels 10; Gaps 2

QY 1 MFTLKKSLLLFLPLGTINISLCEERDADERRDDLEERDV-----EVEKEFFFPVIGRIL 55
DB 1 MFTMRKSLFLPLGTISLCEERSADEGDGEMTEEVKRGILDTLKQFAKGVGKDL 60

QY 56 -----NGIL 59
DB 61 VKGAAGVGL 69

RESULT 10
RN2P RANPI STANDARD; PRT; 71 AA.
AC Q8QFQ4; P82847;
ID 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rana tuerin-2P precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RC Paraghar S.M., Bjourson A.J., Shaw C.;
RA "Cloning of Rana pipiens skin peptides.";
RRL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RRL [2]
RC SEQUENCE OF 45-71, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20117700; PubMed=10651828;
RA Gorsya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
RA Conlon J.M.;
RA "Peptides with antimicrobial activity from four different families
RA isolated from the skins of the North American frogs Rana luteiventris,
RA Rana berlandieri and Rana pipiens.";
RRT Eur. J. Biochem. 267:894-900(2000).
RRL
CC -!- FUNCTION: Antibacterial activity against Gram-positive bacterium
CC S. aureus and Gram-negative bacterium E.coli. Has activity against
CC C.albicans.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=3000.1; METHOD=Electrospray; RANGE=45-71;
CC NOTE=Ref.2.
CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevinin subfamily.
CC -----
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CC -----
CC EMBL; AJ427747; CAD20746.1; -
CC InterPro; IPR004275; Brevenin.
CC Pfam; PF03032; Brevenin; 1.
CC Amphibian defense peptide; Antibiotic; Direct protein sequencing;
CC Fungicide; Signal.
KW SIGNAL 1 20 Potential.
FT PROPEP 21 44 Rana tuerin-2P.
FT PEPTIDE 45 71 By similarity.
FT DISULFID 66 71
SEQUENCE 71 AA; 7941 MW; C871C47FC27FDEF CRC64;

Query Match          47.4%; Score 145; DB 1; Length 71;
Best Local Similarity 50.0%; Pred. No. 6.1e-08;
Matches .30; Conservative 11; Mismatches 17; Indels 2; Gaps 1

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QY 1 MFTLKKSLLLFLGTLINSLCEERDDEERDDLEERDVEVEKRFPPVIGRLNGIIG 60
DB 1 MFTMKSLLLFLGTLINSLCEERDDEERDDLEERDVEVEKRFPPVIGRLNGIIG 58

RESULT 11
PLR_RANPI STANDARD; PRT; 62 AA.
AC Q90MP7; P82110;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peptide leucine arginine precursor (pLR).
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Farragher S., Bjournson A.J., McClean S., Orr D.F., Shaw C.;
RT "Cloning of cDNAs encoding defensive skin secretion peptides from the
RT Northern leopard frog (Rana pipiens).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE OF 44-61, FUNCTION, MASS SPECTROMETRY, DISULFIDE BOND,
RN CIRCULAR DICHROISM ANALYSIS, SYNTHESIS, AND 3D-STRUCTURE MODELING.
RC TISSUE=Skin secretion;
RX MEDLINE=21167822; PubMed=11099505; DOI=10.1074/jbc.M009680200;
RA Salmon A.L., Cross L.J.M., Irvine A.E., Lappin T.R.J., Dache M.,
RA Krause G., Canning P., Thim L., Beyeremann M., Rothemann S.,
RA Bientert M., Shaw C.;
RT "Peptide leucine arginine, a potent immunomodulatory peptide, isolated
RT and structurally characterized from the skin of the Northern Leopard
RT frog, Rana pipiens.";
RL J. Biol. Chem. 276:10145-10152 (2001).
RN [3]
RN FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=98338373; PubMed=9673585;
RA Boyer M., van Den Berg H.W., Shaw C., Lynch M., Johnston P.;
RT "Breast cancer cell lines express specific binding sites for pLR, a
RT novel anti-proliferative peptide from frog skin venom.";
RL Br. J. Cancer 78:41-41 (1998).
RN [4]
RN FUNCTION.
RX PubMed=14636071; DOI=10.1021/bi0345211;
RA Mangoni M.L., Papo N., Mignogna G., Andreu D., Shai Y., Barra D.,
RA Simmaco M.;
RT "Ranacyclins, a new family of short cyclic antimicrobial peptides:
RT biological function, mode of action and parameters involved in target
RT specificity.";
RL Biochemistry 42:14023-14035 (2003).
CC -1- FUNCTION: Mast cell degranulating peptide. Antiproliferative
CC activity against human breast and ovarian tumor cell lines in
CC vitro. Inhibits granulopoiesis in rat in vitro. Causes histamine
CC release from rat peritoneal mast cells in vitro. Has antibacterial
CC activity against Gram-positive bacteria B.megaterium Bm1,
CC S.lentus and M.luteus, and antifungal activity against
CC C.tropicalis, C.guillier-mondii and P.nicotianae spores. Has
CC hemolytic activity. The mature peptide inserts into the
CC hydrophobic core of the bacterial cell membrane and increases
CC permeability without disrupting membrane integrity. Probably binds
CC to the outer membrane surface before aggregating to form
CC transmembrane pores.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- MASS SPECTROMETRY: MW=2136; METHOD=Plasma desorption; RANGE=44-61;
CC NOTE=Ref.2.
CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevinin subfamily.
CC

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EMBL; AJ414584; CAC93861.1; -;
GO; GO:0005576; C:extracellular; IDA.
GO; GO:0005083; P:defense response to fungi; IDA.
GO; GO:0005083; P:defense response to Gram-positive bacteria; IDA.
InterPro; IPR004275; Brevinin.
Pfam; PF03032; Brevinin, 1.
KW Amidation: Amphibian defense peptide; Antibiotic;
KW Cleavage on pair of basic residues; Direct protein sequencing;
KW Fungicide; Hemolysis; Inflammatory response; Mast cell degranulation;
KW Signal.
FT SIGNAL 1 20 Potential.
FT PROPEP 21 41 Peptide leucine arginine.
FT PEPTIDE 44 61
FT DISULFID 48 58
FT MOD_RES 61 61 Arginine amide (G-62 provides amide
group).
SQ SEQUENCE 62 AA; 7113 MW; C8F7F58849A01A1C CRC64;
Query Match 47.1%; Score 144; DB 1; Length 62;
Best Local Similarity 52.6%; Pred. No. 6.8e-08;
Matches 30; Conservative 11; Mismatches 6; Indels 10; Gaps 1;
QY 1 MFTLKKSLLLFLGTLINSLCEERDDEERDDLEERDVEVEKRFPPVIGRLNGIIG 57
DB 1 MFTLKKSLLLFLGTLINSLCEERDDEERDDLEERDVEVEKRFPPVIGRLNGIIG 47

RESULT 12
BRTA_RANPI STANDARD; PRT; 74 AA.
AC P82268;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Brevinin-2Ta precursor.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Simmaco M., Miele R., Mangoni M.L., Barra D.;
RT "A cDNA clone encoding brevinin 2Ta from Rana temporaria.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Shows antibacterial activity against representative
CC Gram-negative and Gram-positive bacterial species (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevinin subfamily.
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EMBL; AJ251567; CAB61442.1; -;
InterPro; IPR004275; Brevinin.
Pfam; PF03032; Brevinin, 1.
KW Amphibian defense peptide; Antibiotic; Hemolysis; Signal.
FT SIGNAL 1 22 Potential.

```

FT PROPEP      23 39          Brevinin-2Ta.
FT PEPTIDE     42 74          By similarity.
FT DISULFID    68 74
SQ SEQUENCE    74 AA; 8162 MW; 5580FDF790B78F75 CRC64;

Query Match
Best Local Similarity 45.3%; Score 138.5; DB 1; Length 74;
Matches 30; Conservative 6; Mismatches 5; Indels 5; Gaps 1;

QY 1 MFTLKSLLLFFLGLTINSLCEERDADDERDDLEERDVEVEKR 46
Db 1 MFTMKSLLLFFLGLTISLCEERADDERDDGEMTEE-----EKR 41

RESULT 13
ID BR2F_RANES STANDARD; PRT; 74 AA.
AC P82269;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Brevinin-2TB precursor.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 42-74.
RP TISSUE=Skin, and skin secretion;
RC MEDLINE=99266278; PubMed=10333736;
RX DOI=10.1002/(SICI)1097-0282(1998)47:6<435::AID-BTP33.3.CO;2-#;
RA Simmaco M., Mignogna G., Barra D., Bressa F.;
RT "Antimicrobial peptides from amphibian skin: what do they tell us?";
RL Biopolymers 47:435-450(1998).
CC Gram-negative and Gram-positive bacterial activity against representative
CC -!- FUNCTION: Shows antibacterial activity against representative
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevinin subfamily.
CC
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CC
CC EMBL; AJ251566; CAB61445.1; -.
CC InterPro; IPR004275; Brevinin.
CC Pfam; PF03032; Brevinin; 1.
CC KW Amphibian defense peptide; Antibiotic; Direct protein sequencing;
CC Hemolysis; Signal.
CC FT SIGNAL 1 22 Potential.
CC FT PROPEP 23 39 Brevinin-2Tb.
CC FT PEPTIDE 42 74 By similarity.
CC FT DISULFID 68 74
CC SEQUENCE 74 AA; 8193 MW; 5B26718D62B79387 CRC64;

Query Match
Best Local Similarity 45.3%; Score 138.5; DB 1; Length 74;
Matches 30; Conservative 6; Mismatches 5; Indels 5; Gaps 1;

QY 1 MFTLKSLLLFFLGLTINSLCEERDADDERDDLEERDVEVEKR 46
Db 1 MFTMKSLLLFFLGLTISLCEERADDERDDGEMTEE-----EKR 41

RESULT 14
BR2F_RANES STANDARD; PRT; 74 AA.
ID BR2F_RANES
AC P40872;

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DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Brevinin-2EF precursor.
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8401;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Skin;
RC MEDLINE=94216303; PubMed=8163497;
RA Simmaco M., Mignogna G., Barra D., Bressa F.;
RT "Antimicrobial peptides from skin secretions of Rana esculenta.
RT Molecular cloning of cDNAs encoding esculentin and brevinins and
RT Isolation of new active peptides.";
RL J. Biol. Chem. 269:11956-11961(1994).
CC -!- FUNCTION: Shows antibacterial activity against representative
CC Gram-negative and Gram-positive bacterial species, and hemolytic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevinin subfamily.
CC
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CC
CC EMBL; X77832; CAAS4843.1; -.
CC InterPro; IPR004275; Brevinin.
CC Pfam; PF03032; Brevinin; 1.
CC KW Amphibian defense peptide; Antibiotic; Hemolysis; Signal.
CC FT SIGNAL 1 22 Potential.
CC FT PROPEP 23 39 Brevinin-2EF.
CC FT PEPTIDE 42 74 By similarity.
CC FT DISULFID 68 74
CC SEQUENCE 74 AA; 8134 MW; 48044D3F01E6D78D CRC64;

Query Match
Best Local Similarity 44.9%; Score 137.5; DB 1; Length 74;
Matches 29; Conservative 8; Mismatches 4; Indels 5; Gaps 1;

QY 1 MFTLKSLLLFFLGLTINSLCEERDADDERDDLEERDVEVEKR 46
Db 1 MFTMKSLLLFFLGLTISLCEERADDERDDGEMTEE-----EKR 41

RESULT 15
ID RAYT_RANES STANDARD; PRT; 62 AA.
AC P83719;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ranacyclin T precursor.
GN Name=RNCT;
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RP TISSUE=Skin;
RC PubMed=14636071; DOI=10.1021/bi034521l;
RA Mangoni M.L., Papo N., Mignogna G., Andreu D., Shai Y., Barra D.,
RA Simmaco M.;
RT "Ranacyclins, a new family of short cyclic antimicrobial peptides:

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RT biological function, mode of action and parameters involved in target
RT specificity."
RL Biochemistry 42:14023-14035(2003).
CC -|- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria B.megaterium Bm11, S.lentus and M.luteus, and Gram-
CC negative bacteria E.coli D22, Y.pseudotuberculosis YP III and
CC P.syringae pv tabaci, and antifungal activity against C.albicans
CC ATCC 10231, C.tropicalis, C.guilliermondii and P.nicotianae
CC spores. Has weak hemolytic activity. The mature peptide inserts
CC into the hydrophobic core of the bacterial cell membrane and
CC increases permeability without disrupting membrane integrity.
CC Probably binds to the outer membrane surface before aggregating to
CC form transmembrane pores.
CC -|- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -|- TISSUE SPECIFICITY: Expressed by the skin granular glands.
CC -|- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevinin subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AJ583866; CAE48162.1; -.
DR InterPro: IPR004275; Brevinin.
KW Amidation; Amphibian defense peptide; Antibiotic;
KW Cleavage on pair of basic residues; Fungicide; Hemolysis; Signal.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 43 Potential.
FT CHAIN 44 60 Banacyclin T.
FT DISULFID 49 59 By similarity.
FT MOD RES 60 60 Lysine amide (G-61 provides amide group).
SQ SEQUENCE 62 AA; 6983 MW; 55A4283837A11E82 CRC64;

Query Match 44.4%; Score 136; DB 1; Length 62;
Best Local Similarity 61.9%; Pred.No.4.8e-07;
Matches 26; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 MFTLKSLLLPFLGTINISLCEERDADAEERDDLEERDVE 42
Db 1 MFTMKKTLLVLPFLGVVSLSLCVERDADEEDGGVEVMEEVK 42

Search completed: March 30, 2005, 17:29:54
Job time : 184 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 17:20:45 ; Search time 43 Seconds
(without alignments)
136.494 Million cell updates/sec

Title: US-10-719-623A-16
Perfect score: 306
Sequence: 1 MFTLKSLLLFLGTINLS.....EVEKRFPPVIGRLINGILCK 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR 79:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	212	69.3	66	1 A53744	ranalexin precursor
2	211.5	69.1	71	2 C53578	brevinin-1Ec precursor
3	189.5	61.9	65	2 S59962	antimicrobial pept
4	148	48.4	80	2 S59961	antimicrobial pept
5	137.5	44.9	74	2 B53578	brevinin-2Ef precursor
6	120	39.2	84	2 A53578	esculentin-1b precursor
7	103	33.7	78	2 B54897	dermaseptin b I precursor
8	103	33.7	81	1 JN0462	dermaseptin b I precursor
9	99.5	32.5	74	2 T10456	dermaseptin B3 precursor
10	99.5	32.5	198	2 B27784	dermorphin precursor
11	98	32.0	197	1 A27784	dermorphin precursor
12	96	31.4	227	2 A35514	[D-Ala(2)] deitorp
13	70.5	23.0	645	1 A23723	protein disulfide
14	70	22.9	429	2 F71896	hypothetical prote
15	69.5	22.7	213	2 G69890	hypothetical prote
16	69	22.5	1512	2 G85090	hypothetical prote
17	68	22.2	313	2 B96892	hypothetical prote
18	66	21.6	436	2 B23364	procaerulein precursor
19	66	21.6	429	2 E64617	hypothetical prote
20	65	21.2	185	2 G70425	hypothetical prote
21	65	21.2	188	2 A23364	caerulein precursor
22	64.5	21.1	361	2 A96261	hypothetical prote
23	64.5	21.1	361	2 AH3023	efflux protein, [hm
24	64	20.9	833	2 T22139	hypothetical prote
25	64	20.9	1684	2 T02367	hypothetical prote
26	63	20.6	490	2 A86265	Cytochrome P450 71
27	62.5	20.4	763	2 A49321	amyloid beta (A4)
28	62	20.3	84	2 AG3788	hypothetical prote
29	62	20.3	201	2 A86363	protein F26H11.1 [

30	62	20.3	241	2 T51964	probable ubiquitin
31	62	20.3	244	2 T21434	hypothetical prote
32	62	20.3	316	2 G96513	hypothetical prote
33	62	20.3	1110	2 I51116	NF-180 - sea lamp
34	61.5	20.1	630	2 S29796	hypothetical prote
35	61.5	20.1	721	2 S29795	hypothetical prote
36	61	19.9	1198	2 D96723	hypothetical prote
37	60.5	19.8	172	2 G70234	conserved hypot
38	60	19.6	81	2 T48398	hypothetical prote
39	60	19.6	150	2 F75070	hypothetical prote
40	60	19.6	289	2 D69152	hypothetical prote
41	60	19.6	678	2 A54514	glutamic acid-rich
42	60	19.6	1430	2 T21910	hypothetical prote
43	59.5	19.4	166	2 A72363	3-isopropylmalate
44	59.5	19.4	232	2 F84798	hypothetical prote
45	59.5	19.4	296	2 A41730	nucleophosmin NO38

ALIGNMENTS

RESULT 1

A53744
ranalexin precursor - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A53744
J:Clark, D.P.; Durell, S.; Maloy, W.L.; Zasloff, M.
J: Biol. Chem. 269, 10849-10855, 1994
A:Title: Ranalexin. A novel antimicrobial peptide from bullfrog (Rana catesbeiana) skin.
A:Reference number: A53744; MUID:94193792; PMID:8144672
A:Accession: A53744
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-66 <CLA>
A:Cross-references: UNIPROT:P39084; GB:S69903; NID:G546211; PIDN:AAB30394.1; PID:G546212
C:Superfamily: ranalexin precursor; dermorphin precursor amino-terminal homology
C:Keywords: disulfide bond; skin
F:1-46/Domain: dermorphin precursor amino-terminal homology <DER>
F:47-66/Product: ranalexin #status experimental <MAT>
F:60-66/Disulfide bonds: #status experimental

Query Match 69.3%; Score 212; DB 1; Length 66;
Best Local Similarity 72.9%; Pred. No. 1.6e-16;
Matches 43; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 MFTLKSLLLFLGTINLSLCEERDADDERDDLEERDVEVERKFFPVIGRLINGIL 59
|||||
Db 1 MFTLKSLLLFLGTINLSLCEERDADDERDDLEERDVEVERKFFPVIGRLINGIL 59

RESULT 2

C53578
brevinin-1Ec precursor - edible frog
A:Alternate names: antimicrobial peptide brevinin 1B
C:Species: Rana esculenta (edible frog)
C>Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C:Accession: C53578; S33729
R:Simmaco, M.; Mignogna, G.; Barra, D.; Bossa, F.
J: Biol. Chem. 269, 11956-11961, 1994
A:Title: Antimicrobial peptides from skin secretions of Rana esculenta. Molecular cloning
A:Reference number: A53578; MUID:94216303; PMID:8163497
A:Accession: C53578
A:Molecule type: mRNA
A:Residues: 1-71 <STM>
A:Cross-references: UNIPROT:P32412; GB:X77831; NID:G488372; PIDN:CAA54842.1; PID:G140579;
R:Simmaco, M.; Mignogna, G.; Barra, D.; Bossa, F.
FEBS Lett. 324, 159-161, 1993
A:Title: Novel antimicrobial peptides from skin secretion of the European frog Rana escul
A:Reference number: S33729; MUID:93285327; PMID:8508915
A:Accession: S33729
A:Molecule type: Protein
A:Residues: 48-71 <SIW>

A:Molecule type: mRNA
A:Residues: 1-81 <AMI>
A:Cross-references: UNIPROT:P31107; EMBL:X70278; NID:G395931; PIDN:CAA49763.1; PID:G395931;
A:Experimental source: skin
A:Note: the authors translated the codon AAA for residue 26 as Leu
R:Amiche, M.; Ducancel, F.; Mor, A.; Boulain, J.C.; Menez, A.; Nicolas, P.
J. Biol. Chem. 269, 17847-17852, 1994
A:Title: Precursors of vertebrate peptide antibiotics dermaseptin b and adenoregulin hav:
A:Reference number: A54897; MUID:94299491; PMID:8074751
A:Accession: A54897
A:Molecule type: mRNA
A:Residues: 1-81 <AMI>
A:Cross-references: GB:X70278; NID:G395931; PIDN:CAA49763.1; PID:G395932
R:Daly, J.W.; Caceres, J.; Moni, R.W.; Gusovsky, F.; Moos Jr., M.; Seamon, K.B.; Milton,
Proc. Natl. Acad. Sci. U.S.A. 89, 10960-10963, 1992
A:Title: Frog secretions and hunting magic in the upper Amazon: identification of a pept
A:Reference number: A44171; MUID:93066363; PMID:1438301
A:Accession: A44171
A:Molecule type: protein
A:Residues: 46-78 <DAL>
C:Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology
C:Keywords: antibiotic; antifungal; skin
F:1-45/Domain: dermorphin precursor amino-terminal homology <DER>
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-45/Domain: propeptide #status predicted <PRO>
F:46-78/Product: adenoregulin #status experimental <MAT>
Query Match 33.7%; Score 103; DB 1; Length 81;
Best Local Similarity 47.7%; Pred. No. 0.00018;
Matches 21; Conservative 12; Mismatches 9; Indels 2; Gaps 1;
QY 1 MFTLKSKLLLLFFGTGTLNLSCEER--DADEERDDLEERDVE 42
DB 1 MAFLKKSFLVFLGLVSLSCIEEKRENEDEEEDDEQSEMK 44
RESULT 9
T10456
dermaseptine B3 precursor - two-colored leaf frog
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10456
R:Charpentier, S.; Amiche, M.; Mester, J.; Vouille, V.; Le Caer, J.P.; Nicolas, P.; Dell
J. Biol. Chem. 273, 14690-14697, 1998
A:Title: Structure, synthesis, and molecular cloning of dermaseptins B, a family of skin
A:Reference number: Z10727; MUID:98278974; PMID:9614066
A:Accession: T10456
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-74 <CHA>
A:Cross-references: UNIPROT:P81485; EMBL:Y16564; NID:G3256036; PIDN:CAA76288.1; PID:G3256
C:Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-74/Product: dermaseptine B3 #status predicted <MAT>
Query Match 32.5%; Score 99.5; DB 2; Length 74;
Best Local Similarity 45.8%; Pred. No. 0.00041;
Matches 22; Conservative 13; Mismatches 8; Indels 5; Gaps 2;
QY 1 MFTLKSKLLLLFFGTGTLNLSCEER--DADEERDDLEERDVEVKR 46
DB 1 MAFLKKSFLVFLGLVSLSCIEEKRENEEKEQDEQSE---EKR 45
RESULT 10
B27784
dermorphin precursor 2 - Sauvage's leaf frog (fragment)
N:Contains: dermorphin
C:Species: Phyllomedusa sauvagei (Sauvage's leaf frog)
C:Date: 31-Mar-1998 #sequence_revision 31-Mar-1998 #text_change 09-Jul-2004
C:Accession: B27784
R:Richter, K.; Eger, R.; Kreil, G.

Science 238, 200-202, 1987
A:Title: D-alanine in the frog skin peptide dermorphin is derived from L-alanine in the
A:Reference number: A94297; MUID:88017999; PMID:3659910
A:Accession: B27784
A:Molecule type: mRNA
A:Residues: 1-198 <RIC>
A:Cross-references: UNIPROT:P05421; GB:M18030; NID:G213542; PID:AAA49452.1; PID:G213543
C:Comment: The precursor contains tandem repeats separated by paired basic residues as in vity.
C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide; skin; tandem repeat
F:1-47/Domain: dermorphin precursor amino-terminal homology <DER>
F:56-62/Domain: dermorphin repeat <RPT1>
F:48-54/Product: dermorphin #status experimental <DER1>
F:83-98/Domain: dermorphin repeat <RPT2>
F:83-99/Product: dermorphin #status experimental <DER2>
F:99-133/Domain: dermorphin repeat <RPT3>
F:118-124/Product: dermorphin #status experimental <DER3>
F:134-168/Domain: dermorphin repeat <RPT4>
F:153-159/Product: dermorphin #status experimental <DER4>
F:169-198/Domain: dermorphin repeat (partial) <RPT5>
F:188-194/Product: dermorphin #status experimental <DER5>
F:54/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly
F:84/Modified site: D-alanine (Ala) #status experimental
F:89/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly
F:119/Modified site: D-alanine (Ala) #status experimental
F:124/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly
F:154/Modified site: D-alanine (Ala) #status experimental
F:159/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly
F:189/Modified site: D-alanine (Ala) #status experimental
F:194/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly

Query Match 32.5%; Score 99.5; DB 2; Length 198;
Best Local Similarity 45.8%; Pred. No. 0.001;
Matches 22; Conservative 10; Mismatches 15; Indels 1; Gaps 1;
A: 1 MFTLKSLLLFLGLTINSLCEERDADERDDLEERDVEVE-KRF 47
B: 1 MSFLKSLLLFLGLVSLVCKEERKRETEENENEENHEGSEMKRYM 48

RESULT 11
A27784
N:Contains: dermorphin precursor 1 - Sauvage's leaf frog
C:Species: Phyllomedusa sauvagei (Sauvage's leaf frog)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A27784; A60595
R:Richter, K.; Egger, R.; Kreil, G.
Science 238, 200-202, 1987
A:Title: D-alanine in the frog skin peptide dermorphin is derived from L-alanine in the
A:Reference number: A94297; MUID:88017999; PMID:3659910
A:Accession: A27784
A:Molecule type: mRNA
A:Residues: 1-197 <RIC>
A:Cross-references: UNIPROT:P05422; GB:M18031; NID:G213544; PID:AAA49453.1; PID:G213545
R:Kreil, G.; Barra, D.; Simmaco, M.; Erspamer, V.; Erspamer, G.F.; Negri, L.; Severini, Eur. J. Pharmacol. 162, 123-128, 1989
A:Title: Deltorphin, a novel amphibian skin peptide with high selectivity and affinity f
A:Reference number: A60595; MUID:89251774; PMID:2542051
A:Accession: A60595
A:Molecule type: protein
A:Residues: 48-54 <KRE>
C:Comment: The precursor contains tandem repeats separated by paired basic residues as i
vity.
C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide; skin; tandem repeat
F:1-47/Domain: dermorphin precursor amino-terminal homology <DER1>
F:1-22/Domain: signal sequence #status predicted <SIG>
F:26-60/Domain: dermorphin repeat <RPT1>
F:48-54/Product: dermorphin #status experimental <DLT>
F:61-95/Domain: dermorphin repeat <RPT2>
F:69-114/Domain: dermorphin precursor amino-terminal homology <DER2>

F:80-86/Product: dermorphin #status experimental <MAT1>
F:96-130/Domain: dermorphin repeat <RPT3>
F:115-121/Product: dermorphin #status experimental <MAT2>
F:131-165/Domain: dermorphin repeat <RPT4>
F:150-156/Product: dermorphin #status experimental <MAT3>
F:166-197/Domain: dermorphin repeat <RPT5>
F:49/Modified site: D-methionine (Met) #status experimental <MAT4>
F:185-191/Product: dermorphin #status experimental
F:54/Modified site: amidated carboxyl end (Asp) (amide in mature form from following gly
F:81/Modified site: D-alanine (Ala) #status experimental
F:86/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly
F:116/Modified site: D-alanine (Ala) #status experimental
F:121/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly
F:151/Modified site: D-alanine (Ala) #status experimental
F:156/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly
F:186/Modified site: D-alanine (Ala) #status experimental
F:191/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly

Query Match 32.0%; Score 98; DB 1; Length 197;
Best Local Similarity 44.0%; Pred. No. 0.0015;
Matches 22; Conservative 11; Mismatches 15; Indels 2; Gaps 1;
A: 1 MFTLKSLLLFLGLTINSLCEERDADERDDLE--ERDVEVEKRF 48
B: 1 MSFLKSLLLFLGLVSLVCKEERKRETEENENEENHEGSEMKRYM 50

RESULT 12
A35514
[D-Ala(2)] deltorphin precursor - two-colored leaf frog
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 31-Oct-1990 #sequence_revision 31-Oct-1990 #text_change 09-Jul-2004
C:Accession: A35514
R:Richter, K.; Egger, R.; Negri, L.; Corsi, R.; Severini, C.; Kreil, G.
Proc. Natl. Acad. Sci. U.S.A. 87, 4836-4839, 1990
A:Title: cDNAs encoding [D-Ala(2)]deltorphin precursors from skin of Phyllomedusa bicolor
A:Reference number: A35514; MUID:90280471; PMID:2352951
A:Accession: A35514
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-227 <RIC>
A:Cross-references: UNIPROT:P21850; GB:M34560; NID:G213540; PID:AAA49451.1; PID:G213541
C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
F:1-48/Domain: dermorphin precursor amino-terminal homology <DER1>
F:168-214/Domain: dermorphin precursor amino-terminal homology <DER2>

Query Match 31.4%; Score 96; DB 2; Length 227;
Best Local Similarity 46.9%; Pred. No. 0.0029;
Matches 23; Conservative 11; Mismatches 13; Indels 2; Gaps 2;
A: 1 MFTLKSLLLFLGLTINSLC-EERDADERDDLEERDVEVE-KRF 47
B: 1 MSFLKSLLLFLGLVSHSVCKEERKRETEENENEENHEGSEMKRY 49

RESULT 13
A23723
protein disulfide-isomerase (EC 5.3.4.1) Erp72 precursor - human
N:Alternate names: endoplasmic reticulum protein Erp72
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A23723; A36508
R:Huang, S.H.; Tomich, J.W.; Wu, H.; Jong, A.; Holcenberg, J.
J. Biol. Chem. 266, 5353, 1991
A:Reference number: A23723; MUID:91161636; PMID:2002068
A:Content: erratum
A:Accession: A23723
A:Molecule type: mRNA
A:Residues: 1-645 <HUA>
A:Cross-references: UNIPROT:P13667; GB:J05016; NID:G181507; PID:AAA58460.1; PID:G181508
R:Huang, S.H.; Tomich, J.W.; Wu, H.; Jong, A.; Holcenberg, J.
J. Biol. Chem. 264, 14762-14768, 1989

A;Title: Human deoxycytidine kinase. Sequence of cDNA clones and analysis of expression
 A;Reference number: A36508; MUID:89359272; PMID:2549034
 A;Accession: A36508
 A;Molecule type: DNA
 A;Residues: 1-609; 'TKRTQLNRVETEWSI' <HU2>
 A;Cross-references: GB:J05016
 A;Note: this sequence has been corrected reference A23723
 C;Comment: This sequence has no homology to deoxycytidine kinase (EC 2.7.1.74) and the P
 C;Genetics:
 A;Gene: GDB:ERP70; ERP72
 A;Cross-references: GDB:9957774
 C;Superfamily: protein disulfide-isomerase; thioredoxin homology
 C;Keywords: duplication; endoplasmic reticulum; intramolecular oxidoreductase; isomerase
 F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-645/Product: endoplasmic reticulum protein ERP72 #status predicted <MAT>
 F;70-154/Domain: thioredoxin homology <TX1>
 F;185-269/Domain: thioredoxin homology <TX2>
 F;533-620/Domain: thioredoxin homology <TX3>
 F;642-645/Region: endoplasmic reticulum retention signal
 F;91-94, 206-209, 555-558/Disulfide bonds: redox-active #status predicted

Query Match 23.0%; Score 70.5; DB 1; Length 645;
 Best Local Similarity 28.2%; Pred. No. 5;
 Matches 20; Conservative 10; Mismatches 16; Indels 25; Gaps 2;
 QY 5 KKSLLLLFLGTTINLSLCE-----EERDADERRDDLEERDVEVEKRPFF 48
 Db 4 RKAFLLLLLGLVQLLAVAGSGPDDSSNRENAIEDEEEEDDDDEEDOLEVKE-- 61
 QY 49 PVIGRIINGIL 59
 Db 62 -----NGVL 65

RESULT 14

F71896
 hypothetical protein jhp0718 - Helicobacter pylori (strain J99)
 C;Species: Helicobacter pylori
 A;Variety: strain J99
 C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 C;Accession: F71896
 R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
 Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
 Nature 397, 176-180, 1999
 A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
 A;Reference number: A71800; MUID:99120557; PMID:9923682
 A;Accession: F71896
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-429 <ARN>
 A;Cross-references: UNIPROT:Q9ZL62; GB:AB001503; GB:AE001439; MUID:g4155275; PIDN:AAD0630
 A;Experimental source: strain J99
 C;Genetics:
 A;Gene: jhp0718

Query Match 22.9%; Score 70; DB 2; Length 429;
 Best Local Similarity 41.3%; Pred. No. 3.8;
 Matches 19; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 10 LLFFLGTINLSCEERDADERRDDLEERDVEVEKRPFPVIGRIIL 55
 Db 130 LLAYLNTRNDNFNIQVFDSESPKLEETYEKEKEKFPFIALL 175

RESULT 15

G69850
 hypothetical protein yjha - Bacillus subtilis
 C;Species: Bacillus subtilis
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C;Accession: G69850
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
 C.; Bron, S.; Brouillet, S.; Bruchchi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
 Y. M.; Ogawa, K.; Ogiwara, C.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
 A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot,
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
 A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A;Reference number: A69580; MUID:98044033; PMID:9384377
 A;Accession: G69850
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-213 <KUN>
 A;Cross-references: UNIPROT:O34725; GB:Z99110; GB:AL009156; MUID:g2633472; PIDN:CAB13075.5
 A;Experimental source: strain 168
 C;Genetics:
 A;Gene: yjha
 C;Superfamily: Bacillus subtilis hypothetical protein yjha

Query Match 22.7%; Score 69.5; DB 2; Length 213;
 Best Local Similarity 43.2%; Pred. No. 2.2;
 Matches 19; Conservative 8; Mismatches 14; Indels 3; Gaps 2;
 QY 4 LKKSLLLLFLGTTINLSL--CEEERDADERRDDLEERDVEVEK 45
 Db 1 MKKVVLLLPVL-TIGLALSACSSSDASEKEKPEKKSQEELEK 43

Search completed: March 30, 2005, 17:30:44
 Job time : 45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 17:30:01 ; Search time 140 Seconds
(without alignments)
144.265 Million cell updates/sec

Title: US-10-719-623A-16

Perfect score: 306

Sequence: 1 MFTLKSLLLFLGTINLS.....EVEKRFPPVIGRLNGILGK 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	306	100.0	61	15	US-10-719-623-16
2	103	33.7	78	15	US-10-719-623-2
3	95	31.0	24	15	US-10-421-635-8
4	70.5	23.0	1039	15	US-10-369-493-16475
5	70	22.9	429	15	US-10-335-977-6289
6	70	22.9	430	15	US-10-335-977-6290
7	67.5	22.1	1189	15	US-10-282-122A-45818
8	66	21.6	13	15	US-10-719-623-17
9	66	21.6	193	15	US-10-424-599-245431
10	65.5	21.4	1192	9	US-10-815-242-10903
11	65.5	21.4	1192	15	US-10-282-122A-57178
12	64	20.9	1684	16	US-10-408-765A-811
13	63	20.6	59	14	US-10-029-386-32735

14	62.5	20.4	705	9	US-09-925-302-531	Sequence 531, App
15	62.5	20.4	705	10	US-09-925-302-531	Sequence 531, App
16	62.5	20.4	763	15	US-10-428-487-9	Sequence 9, Appl
17	62	20.3	403	15	US-10-425-114-39578	Sequence 39578, A
18	62	20.3	549	9	US-09-764-864-1131	Sequence 1131, App
19	62	20.3	576	15	US-10-425-114-65214	Sequence 65214, A
20	62	20.3	586	15	US-10-425-114-70516	Sequence 70516, A
21	62	20.3	708	16	US-10-437-963-167468	Sequence 167468, A
22	61.5	20.1	286	15	US-10-424-599-282549	Sequence 282549, A
23	61	19.9	207	15	US-10-425-114-41590	Sequence 41590, A
24	60	19.6	64	9	US-09-864-761-45501	Sequence 45501, A
25	60	19.6	367	15	US-10-425-114-48334	Sequence 48334, A
26	60	19.6	605	9	US-09-860-298-2	Sequence 2, Appl
27	60	19.6	605	10	US-09-832-129-37	Sequence 37, Appl
28	60	19.6	605	11	US-09-833-245-2237	Sequence 2237, App
29	60	19.6	605	14	US-10-028-072-160	Sequence 160, App
30	60	19.6	605	14	US-10-140-808-160	Sequence 160, App
31	60	19.6	605	14	US-10-121-049-160	Sequence 160, App
32	60	19.6	605	14	US-10-123-904-160	Sequence 160, App
33	60	19.6	605	14	US-10-140-470-160	Sequence 160, App
34	60	19.6	605	14	US-10-175-746-160	Sequence 160, App
35	60	19.6	605	14	US-10-176-918-160	Sequence 160, App
36	60	19.6	605	14	US-10-137-865-160	Sequence 160, App
37	60	19.6	605	14	US-10-140-474-160	Sequence 160, App
38	60	19.6	605	14	US-10-142-431-160	Sequence 160, App
39	60	19.6	605	14	US-10-143-114-160	Sequence 160, App
40	60	19.6	605	14	US-10-142-419-160	Sequence 160, App
41	60	19.6	605	14	US-10-123-262-160	Sequence 160, App
42	60	19.6	605	14	US-10-142-423-160	Sequence 160, App
43	60	19.6	605	14	US-10-121-050-160	Sequence 160, App
44	60	19.6	605	14	US-10-141-755-160	Sequence 160, App
45	60	19.6	605	14	US-10-141-755-160	Sequence 160, App

ALIGNMENTS

RESULT 1

US-10-719-623-16

; Sequence 16, Application US/10719623

; Publication No. US20040073977A1

; GENERAL INFORMATION:

; APPLICANT: Miera and Kay

; TITLE OF INVENTION: Transgenic Plants that are Resistant to a Broad Spectrum

; FILE OF INVENTION: Of Pathogens

; FILE REFERENCE: 673243

; CURRENT APPLICATION NUMBER: US/10/719,623

; PRIOR FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/125,072

; PRIOR FILING DATE: 1999-03-17

; PRIOR APPLICATION NUMBER: PCT/CA00/00288

; PRIOR FILING DATE: 2000-03-16

; PRIOR APPLICATION NUMBER: 09/936,885

; PRIOR FILING DATE: 2001-09-17

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 16

; LENGTH: 61

; TYPE: PRT

; ORGANISM: Rana temporaria

US-10-719-623-16

Query Match 100.0%; Score 306; DB 15; Length 61;

Best Local Similarity 100.0%; Pred. No. 5.3e-29;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFTLKSLLLFLGTINLSLCEERDADDEERDDLEERDVEVEKRFPPVIGRLNGILG 60

Db 1 MFTLKSLLLFLGTINLSLCEERDADDEERDDLEERDVEVEKRFPPVIGRLNGILG 60

Qy 61 K 61

Db 61 K 61


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RESULT 2
US-10-719-623-2
; Sequence 2, Application US/10719623
; Publication No. US20040073977A1
; GENERAL INFORMATION:
; APPLICANT: Miera and Kay
; TITLE OF INVENTION: Transgenic Plants that are Resistant to a Broad Spectrum
; TITLE OF INVENTION: of Pathogens
; FILE REFERENCE: 673243
; CURRENT APPLICATION NUMBER: US/10/719,623
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/125,072
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: PCT/CA00/00288
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 09/936,885
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Phyllomedusa bicolor
US-10-719-623-2
Query Match 33.7%; Score 103; DB 15; Length 78;
Best Local Similarity 56.8%; Pred. No. 0.00011;
Matches 21; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

QY 1 MFTLKSLLLPLGLTINLSLCEER--DADERDD 35
Db 1 MDILKSLFLVLPLGLVLSLCEERKRENEDEKQDD 37

RESULT 3
US-10-421-635-8
; Sequence 8, Application US/10421635
; Publication No. US20040064847A1
; GENERAL INFORMATION:
; APPLICANT: Miera, Santosh et al.
; TITLE OF INVENTION: Transgenic Plants Exhibiting Resistance to a Spectrum
; FILE REFERENCE: 55682
; CURRENT APPLICATION NUMBER: US/10/421,635
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: US/09/616,110
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/165,249
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; TYPE: PRT
; ORGANISM: Rana temporaria
US-10-421-635-8
Query Match 31.0%; Score 95; DB 15; Length 24;
Best Local Similarity 75.0%; Pred. No. 0.00025;
Matches 18; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 23 EERDADEERRDDLEERDVEVEKR 46
Db 1 EEERNAEEERDDPDERDQVEKR 24

RESULT 4
US-10-369-493-16475
; Sequence 16475, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16475
; LENGTH: 1039
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(1039)
; OTHER INFORMATION: unsure at all xaa locations
US-10-369-493-16475
Query Match 23.0%; Score 70.5; DB 15; Length 1039;
Best Local Similarity 41.2%; Pred. No. 16;
Matches 21; Conservative 6; Mismatches 7; Indels 17; Gaps 3;

QY 14 LGTINLSLCEER-ERDADE-----ERRDLE-----ERDVEVEKRF 47
Db 837 LGTNLGAIDERYVAERHTFLLEQRDDLEAKATLHQLITMDEMKCRF 887

RESULT 5
US-10-335-977-6289
; Sequence 6289, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 6289:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 429 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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QY 10 LLFFLGTINLSLCEEERDADEERRDDLEERDVEVEKRRFFPVIGRIL 55

QY 10 LLFFLGTINLSLCEEERDADEERRDDLEERDVEVEKRRFFPVIGRIL 55

FILE REFERENCE: 673243
CURRENT APPLICATION NUMBER: US/10/719.623

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57178
; LENGTH: 1192
; TYPE: PR
; ORGANISM: Enterococcus faecalis
US-10-282-122A-57178

Query Match      21.4%; Score 65.5; DB 15; Length 1192;
Best Local Similarity 34.5%; Pred. No. 74;
Matches 20; Conservative 6; Mismatches 15; Indels 17; Gaps 2;

QY 14 LGTNLSLCEERDADS-----ERDDL-----EERDVVEKRPFPVIGRI 54
Db 984 LGPNLSAIEQFQVDERHQFLVSQRDLDLNAKEQLFETWDEMDQVKRKFVFEAI 1041

RESULT 12
US-10-408-765A-811
; Sequence 811, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Pabhy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 811
; LENGTH: 1684
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-408-765A-811

Query Match      20.9%; Score 64; DB 16; Length 1684;
Best Local Similarity 54.2%; Pred. No. 1.7e+02;
Matches 13; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 23 EERDADEERRDDLEERDVVEKRP 46
Db 113 EEEEEDEERKSDERQKKKKR 136

RESULT 13
US-10-029-386-32735
; Sequence 32735, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32735
; LENGTH: 59
; TYPE: PR
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004493.1
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; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.5
US-10-029-386-32735

Query Match      20.6%; Score 63; DB 14; Length 59;
Best Local Similarity 40.0%; Pred. No. 4.5;
Matches 12; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 23 EERDADEERRDDLEERDVVEKRPFPVIG 52
Db 25 EEEEEEEDEEELELELELLERLPLAG 54

RESULT 14
US-09-925-302-531
; Sequence 531, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 531
; LENGTH: 705
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-925-302-531

Query Match      20.4%; Score 62.5; DB 9; Length 705;
Best Local Similarity 51.9%; Pred. No. 91;
Matches 14; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 23 EERDADEERRDDLEERDVVEKRPFP 49
Db 226 EEEEEEEED-EEEDYDVYKSEFP 251

RESULT 15
US-09-925-302-531
; Sequence 531, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 531
; LENGTH: 705
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-925-302-531

Query Match      20.4%; Score 62.5; DB 10; Length 705;
Best Local Similarity 51.9%; Pred. No. 91;
Matches 14; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 23 EERDADEERRDDLEERDVVEKRPFP 49
Db 226 EEEEEEEED-EEEDYDVYKSEFP 251
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Search completed: March 30, 2005, 17:42:51
Job time : 141 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 17:21:25 ; Search time 42 Seconds
(without alignments)
108.419 Million cell updates/sec

Title: US-10-719-623A-16
Perfect score: 306
Sequence: 1 MFTLKXSLLLFFLTGTLNLS.....EVEKRFPPVIGRLNGILGK 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCITUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	306	100.0	61	3	US-09-319-730-19
2	306	100.0	61	4	US-09-936-885A-16
3	245	80.1	61	3	US-09-319-730-15
4	219.5	71.7	58	3	US-09-319-730-17
5	103	33.7	78	4	US-09-936-885A-2
6	70.5	23.0	645	4	US-09-538-092-920
7	66	21.6	13	3	US-09-319-730-7
8	66	21.6	13	4	US-09-936-885A-17
9	65.5	21.4	1208	4	US-09-134-000C-5756
10	62.5	20.4	166	4	US-09-513-999C-5648
11	62.5	20.4	706	1	US-08-339-152A-29
12	62.5	20.4	706	2	US-08-007-999B-4
13	62.5	20.4	706	2	US-08-689-276A-4
14	62.5	20.4	763	1	US-08-155-331-13
15	62.5	20.4	763	1	US-08-424-022-13
16	62.5	20.4	763	2	US-08-424-017B-13
17	62.5	20.4	763	4	US-09-538-092-1272
18	62.5	20.4	763	5	PCT-US93-11696-13
19	62	20.3	932	4	US-09-248-796A-19128
20	61	19.9	95	3	US-09-134-001C-5627
21	60.5	19.8	103	3	US-09-134-001C-4292
22	60	19.6	605	3	US-09-394-645-2
23	60	19.6	605	3	US-09-243-560B-2
24	60	19.6	3457	2	US-08-416-603-4
25	59.5	19.4	180	4	US-09-569-804-35
26	59.5	19.4	161	4	US-09-107-532A-4446
27	59.5	19.4	462	4	US-09-543-681A-5241

28 59.5 19.4 576 4 US-09-519-232-4 Sequence 4, Appli
29 58.5 19.1 608 4 US-09-270-767-3937 Sequence 3237, A
30 58.5 19.1 608 4 US-09-270-767-48154 Sequence 48154, A
31 58 19.0 388 4 US-09-248-796A-18781 Sequence 18781, A
32 58 19.0 590 4 US-09-248-796A-18990 Sequence 18990, A
33 58 19.0 1898 1 US-08-056-200-94 Sequence 94, Appl
34 58 19.0 1898 2 US-08-800-644-94 Sequence 94, Appl
35 58 19.0 1898 4 US-09-538-092-1280 Sequence 1280, Ap
36 57.5 18.8 822 4 US-09-328-352-5754 Sequence 5754, Ap
37 57.5 18.8 1382 4 US-09-171-991-9 Sequence 9, Appli
38 57.5 18.8 1388 4 US-09-949-016-10817 Sequence 10817, A
39 57 18.6 61 4 US-09-248-796A-25881 Sequence 25881, A
40 57 18.6 87 4 US-09-248-796A-22150 Sequence 22150, A
41 57 18.6 183 4 US-09-107-532A-5644 Sequence 5644, Ap
42 57 18.6 315 4 US-09-585-645A-42 Sequence 42, Appl
43 57 18.6 437 4 US-09-538-092-876 Sequence 876, App
44 57 18.6 568 4 US-09-949-016-10896 Sequence 10896, A
45 57 18.6 587 4 US-09-538-092-1130 Sequence 1130, Ap

ALIGNMENTS

RESULT 1
US-09-319-730-19
; Sequence 19, Application US/09319730
; Patent No. 6310176
; GENERAL INFORMATION:
; APPLICANT: BARRA, Donatella
; APPLICANT: SIMMACO, Maurizio
; TITLE OF INVENTION: ANTIMICROBIALY ACTIVE POLYPEPTIDES
; FILE REFERENCE: 00300-574
; CURRENT APPLICATION NUMBER: US/09/319,730
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: PCT/SE97/02075
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: SE 9604593-5
; PRIOR FILING DATE: 1996-12-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Rana Temporaria
US-09-319-730-19

Query Match 100.0%; Score 306; DB 3; Length 61;
Best Local Similarity 100.0%; Pred. No. 7.8e-31;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFTLKXSLLLFFLTGTLNLSLCEERDADEERDDLEERDVEKRFPPVIGRLNGILG 60
Db 1 MFTLKXSLLLFFLTGTLNLSLCEERDADEERDDLEERDVEKRFPPVIGRLNGILG 60
Qy 61 K 61
Db 61 K 61

RESULT 2
US-09-936-885A-16
; Sequence 16, Application US/09936885A
; Patent No. 6835868
; GENERAL INFORMATION:
; APPLICANT: Misra and Kay
; TITLE OF INVENTION: Transgenic Plants that are Resistant to a Broad Spectrum
; TITLE OF INVENTION: of Pathogens
; FILE REFERENCE: 60993
; CURRENT APPLICATION NUMBER: US/09/936,885A
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/125,072
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: PCT/CA00/00288

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; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Rana temporaria
US-09-936-885A-16

Query Match
Best Local Similarity 100.0%; Score 306; DB 4; Length 61;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFTLKSLLLFLPLGTINLSLCEERDADERRDDLEERDVEVEKRFPPVIGRIILNGILG 60
Db 1 MFTLKSLLLFLPLGTINLSLCEERDADERRDDLEERDVEVEKRFPPVIGRIILNGILG 60

QY 61 K 61
Db 61 K 61

RESULT 3
US-09-319-730-15
; Sequence 15, Application US/09319730
; Patent No. 6310176
; GENERAL INFORMATION:
; APPLICANT: BARRA, Donatella
; APPLICANT: SIMMACO, Maurizio
; TITLE OF INVENTION: ANTIMICROBIALY ACTIVE POLYPEPTIDES
; FILE REFERENCE: 003300-574
; CURRENT APPLICATION NUMBER: US/09/319,730
; CURRENT FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: PCT/SE97/02075
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: SE 9604593-5
; PRIOR FILING DATE: 1996-12-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Rana Temporaria
US-09-319-730-15

Query Match
Best Local Similarity 80.1%; Score 245; DB 3; Length 61;
Matches 46; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 MFTLKSLLLFLPLGTINLSLCEERDADERRDDLEERDVEVEKRFPPVIGRIILNGILG 60
Db 1 MFTLKSLLLFLPLGTINLSLCEERDADERRDDLEERDVEVEKRFPPVIGRIILNGILG 60

QY 61 K 61
Db 61 K 61

RESULT 4
US-09-319-730-17
; Sequence 17, Application US/09319730
; Patent No. 6310176
; GENERAL INFORMATION:
; APPLICANT: BARRA, Donatella
; APPLICANT: SIMMACO, Maurizio
; TITLE OF INVENTION: ANTIMICROBIALY ACTIVE POLYPEPTIDES
; FILE REFERENCE: 003300-574
; CURRENT APPLICATION NUMBER: US/09/319,730
; CURRENT FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: PCT/SE97/02075
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: SE 9604593-5
; PRIOR FILING DATE: 1996-12-13

; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Rana Temporaria
US-09-319-730-17

Query Match
Best Local Similarity 71.7%; Score 219.5; DB 3; Length 58;
Matches 45; Conservative 7; Mismatches 6; Indels 3; Gaps 1;

QY 1 MFTLKSLLLFLPLGTINLSLCEERDADERRDDLEERDVEVEKRFPPVIGRIILNGILG 60
Db 1 MFTLKSLLLFLPLGTINLSLCEERDADERRDDLEERDVEVEKRFPPVIGRIILNGILG 57

QY 61 K 61
Db 58 K 58

RESULT 5
US-09-936-885A-2
; Sequence 2, Application US/09936885A
; Patent No. 6835868
; GENERAL INFORMATION:
; APPLICANT: Misra and Kay
; TITLE OF INVENTION: Transgenic Plants that are Resistant to a Broad Spectrum
; FILE OF INVENTION: of Pathogens
; FILE REFERENCE: 60993
; CURRENT APPLICATION NUMBER: US/09/936,885A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/125,072
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: PCT/CA00/00288
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Phyllomedusa bicolor
US-09-936-885A-2

Query Match
Best Local Similarity 33.7%; Score 103; DB 4; Length 78;
Matches 21; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

QY 1 MFTLKSLLLFLPLGTINLSLCEER--DADERRDD 35
Db 1 MDILKSLFLVLFLGLVSLICEEKEKRENEDEKQDD 37

RESULT 6
US-09-538-092-920
; Sequence 920, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 920
; LENGTH: 645
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(6)
; OTHER INFORMATION: Polypeptide Accession Number P13667
US-09-538-092-920

Query Match      23.0%; Score 70.5; DB 4; Length 645;
Best Local Similarity 28.2%; Pred. No. 1.5;
Matches 20; Conservative 10; Mismatches 16; Indels 25; Gaps 2;

QY 5 KKSLLLLFFLGTINLSLCE-----BERDAEERRDDDLERDVEVEKRF 48
Db 4 RKAFLLLLLGLVQLAVAGAGPDESDSSNRNAIDEEEDDEEDDEEDLEVKEE-- 61

QY 49 PVTGRIILNGIL 59
Db 62 -----NGVL 65

RESULT 7
US-09-319-730-7
; Sequence 7, Application US/09319730
; Patent No. 6310176
; GENERAL INFORMATION:
; APPLICANT: BARRA, Donatella
; APPLICANT: SIMMACO, Maurizio
; TITLE OF INVENTION: ANTIMICROBIALY ACTIVE POLYPEPTIDES
; FILE REFERENCE: 003300-574
; CURRENT APPLICATION NUMBER: US/09/319,730
; CURRENT FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: PCT/SE97/02075
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: SE 9604593-5
; PRIOR FILING DATE: 1996-12-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Rana temporaria
US-09-319-730-7

Query Match      21.6%; Score 66; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 FFPVIGRIILNGIL 59
Db 1 FFPVIGRIILNGIL 13

RESULT 8
US-09-936-885A-17
; Sequence 17, Application US/09936885A
; Patent No. 6835868
; GENERAL INFORMATION:
; APPLICANT: Misra and Kay
; TITLE OF INVENTION: Transgenic Plants that are Resistant to a Broad Spectrum
; FILE REFERENCE: 60993
; CURRENT APPLICATION NUMBER: US/09/936,885A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/125,072
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: PCT/CA00/00288
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Rana temporaria

US-09-936-885A-17

Query Match      21.6%; Score 66; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 FFPVIGRIILNGIL 59
Db 1 FFPVIGRIILNGIL 13

RESULT 9
US-09-134-000C-5756
; Sequence 5756, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5756
; LENGTH: 1208
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5756

Query Match      21.4%; Score 65.5; DB 4; Length 1208;
Best Local Similarity 34.5%; Pred. No. 13;
Matches 20; Conservative 6; Mismatches 15; Indels 17; Gaps 2;

QY 14 LGTINLSCEERDADE-----ERRDDU-----ERDVEVEKRFPPVIGRI 54
Db 1000 LGFVNLSAIEQEQVDRHQFLVSQDDLLNNAKEQLFETMDMDQVKEKRFKEVFEAI 1057

RESULT 10
US-09-513-999C-5648
; Sequence 5648, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5648
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 92
; OTHER INFORMATION: Xaa=Asp or Glu
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 94
; OTHER INFORMATION: Xaa=Asp or Glu or Gly
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 126
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; OTHER INFORMATION: Xaa=His or Arg
US-09-513-999C-5648

Query Match      20.4%; Score 62.5; DB 4; Length 166;
Best Local Similarity 51.9%; Pred. No. 3.3;
Matches 14; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 23 EERDAEERDDLEERDVEVEKRFPP 49
Db 38 EEEDEEEEEEED-EEEDYDVYKSEFP 63

RESULT 11
US-08-339-152A-29
; Sequence 25, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,152A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609.4120000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 706 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-339-152A-29

Query Match      20.4%; Score 62.5; DB 1; Length 706;
Best Local Similarity 51.9%; Pred. No. 17;
Matches 14; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 23 EERDAEERDDLEERDVEVEKRFPP 49
Db 217 EEEDEEEEEEED-EEEDYDVYKSEFP 242

RESULT 12
US-08-007-999B-4
; Sequence 4, Application US/08007999B
; Patent No. 5851787
; GENERAL INFORMATION:
; APPLICANT: Wasco, Wilma
; APPLICANT: Bupp, Keith
; APPLICANT: Magendantz, Margaret
; APPLICANT: Tanzi, Rudolph
; APPLICANT: Solomon, Frank
; TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,276A
```

```
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/007,999B
; FILING DATE: 21-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,642
; FILING DATE: 20-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,022
; FILING DATE: 17-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: 0609.3520002/JAG/GKT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2571
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 706 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-007-999B-4

Query Match      20.4%; Score 62.5; DB 2; Length 706;
Best Local Similarity 51.9%; Pred. No. 17;
Matches 14; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 23 EERDAEERDDLEERDVEVEKRFPP 49
Db 217 EEEDEEEEEEED-EEEDYDVYKSEFP 242

RESULT 13
US-08-689-276A-4
; Sequence 4, Application US/08689276A
; Patent No. 5891991
; GENERAL INFORMATION:
; APPLICANT: Wasco, Wilma
; APPLICANT: Bupp, Keith
; APPLICANT: Magendantz, Margaret
; APPLICANT: Tanzi, Rudolph
; APPLICANT: Solomon, Frank
; TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,276A
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; FILING DATE: 06-AUG-1996
; PRIOR APPLICATION DATA: US 08/007,999
; APPLICATION NUMBER:
; FILING DATE: 21-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,642
; FILING DATE: 20-APR-1992
; PRIOR APPLICATION DATA: US 07/930,022
; APPLICATION NUMBER:
; FILING DATE: 17-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0609.3520003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2571
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 706 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-689-276A-4

Query Match 20.4%; Score 62.5; DB 2; Length 706;
Best Local Similarity 51.9%; Pred. No. 17;
Matches 14; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 23 EEERDAEERRDDLEERDVEVEKRFPP 49
Db 217 EEEDEEEEEEED-EEEDYDVYKSEFP 242

RESULT 14
US-08-155-331-13
; Sequence 13, Application US/08155331
; Patent No. 5441931
; GENERAL INFORMATION:
; APPLICANT: Foster, Donald C
; APPLICANT: Sprecher, Cindy
; APPLICANT: No. 5441931ris, Kjeld
; TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR
; TITLE OF INVENTION: HOMOLOG AND KUNITZ-TYPE INHIBITOR
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,331
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,692
; FILING DATE: 02-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31-684
; REFERENCE/DOCKET NUMBER: 92-21C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 322
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 763 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-155-331-13
Query Match 20.4%; Score 62.5; DB 1; Length 763;
Best Local Similarity 51.9%; Pred. No. 18;
Matches 14; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 23 EEERDAEERRDDLEERDVEVEKRFPP 49
Db 216 EEEDEEEEEEED-EEEDYDVYKSEFP 241

RESULT 15
US-08-424-022-13
; Sequence 13, Application US/08424022
; Patent No. 5677146
; GENERAL INFORMATION:
; APPLICANT: Foster, Donald C
; APPLICANT: Sprecher, Cindy
; APPLICANT: No. 5677146ris, Kjeld
; TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR
; TITLE OF INVENTION: HOMOLOG AND KUNITZ-TYPE INHIBITOR
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,022
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,692
; FILING DATE: 02-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31-684
; REFERENCE/DOCKET NUMBER: 92-21C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 322
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 763 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-022-13

Query Match 20.4%; Score 62.5; DB 1; Length 763;
Best Local Similarity 51.9%; Pred. No. 18;
Matches 14; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 23 EEERDAEERRDDLEERDVEVEKRFPP 49
Db 216 EEEDEEEEEEED-EEEDYDVYKSEFP 241

Search completed: March 30, 2005, 17:31:32
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: March 30, 2005, 17:11:55 ; Search time 171 Seconds
(without alignments)
137.967 Million cell updates/sec

Title: US-10-719-623A-16
Perfect score: 306
Sequence: 1 MFTLKSLLLFLFTINLS.....EVEKRPFPVIGRLNGILGK 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 16Dec04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	306	100.0	61	AAW51843	Aaw51843 Rana temp
2	306	100.0	61	AAI18737	Aabi18737 A tempor
3	245	80.1	61	AAW51841	Aaw51841 Rana temp
4	219.5	71.7	58	AAW51842	Aaw51842 Rana temp
5	103	33.7	78	AAI18724	Aabi18724 A dermase
6	95	31.0	24	AAW62384	Aag62384 Pro-regio
7	92	30.1	62	ADR88893	Adr88893 Amino aci
8	70.5	23.0	645	AAW66531	Aag66531 Human int
9	70.5	23.0	645	ADOL19794	Adol19794 Human PRO
10	70.5	23.0	645	ABM80947	Abm80947 Tumour-as
11	70.5	23.0	645	ADP56088	Adp56088 Human PRO
12	70.5	23.0	646	AAU30243	Aau30243 Novel hum
13	70.5	23.0	918	AAU30491	Aau30491 Novel hum
14	70.5	23.0	1039	ADS27442	Ads27442 Bacterial
15	70	22.9	429	AAV10949	Aay10949 H. pylori
16	70	22.9	430	AAW20585	Aaw20585 H. pylori
17	69	22.5	1512	ADM57239	Adm57239 A thalian
18	68	22.2	605	AAV57950	Aay57950 Human tra
19	67.5	22.1	91	AAU30488	Aau30488 Novel hum
20	67.5	22.1	1189	ABU17894	Abu17894 Protein e
21	66	21.6	13	AAI18738	Aabi18738 Amino aci
22	66	21.6	122	ABG03927	Abg03927 Novel hum
23	66	21.6	164	ABG02975	Abg02975 Novel hum
24	66	21.6	164	ABG05363	Abg05363 Novel hum
25	66	21.6	199	ABG06330	Abg06330 Novel hum

26	66	21.6	283	5	ABU52101	Abu52101 Helicobac
27	66	21.6	429	4	AAI46342	Aai46342 H. pylori
28	66	21.6	429	4	AAI46403	Aai46403 H. pylori
29	65.5	21.4	1192	4	AAU35310	Aau35310 Enterococ
30	65.5	21.4	1192	6	ABU29254	Abu29254 Protein e
31	65.5	21.4	1208	7	ADH87871	Adh87871 Enterococ
32	65	21.2	365	4	ABG63283	Abg63283 Drosophil
33	64	20.9	1598	3	AAI30466	Aai30466 Arabidops
34	64	20.9	1599	3	AAI30465	Aai30465 Arabidops
35	64	20.9	1637	3	AAI41602	Aai41602 Arabidops
36	64	20.9	1684	3	AAI30464	Aai30464 Arabidops
37	64	20.9	1684	7	ADJ69005	Adj69005 Human hea
38	63.5	20.8	211	3	AAI3517	Aai3517 Arabidops
39	63.5	20.8	219	3	AAI23516	Aai23516 Arabidops
40	63.5	20.8	309	3	AAI23515	Aai23515 Arabidops
41	63.5	20.8	2478	4	ABG64182	Abg64182 Drosophil
42	63	20.6	59	8	ABO59101	Abos59101 Human gen
43	63	20.6	106	4	ABG68525	Abg68525 Drosophil
44	63	20.6	368	3	AAI44390	Aai44390 Arabidops
45	63	20.6	465	3	AAI44389	Aai44389 Arabidops

ALIGNMENTS

RESULT 1
AAW51843
ID AAW51843 standard; protein; 61 AA.

XX AAW51843;

XX 26-OCT-1998 (first entry)

XX Rana temporaria temporin G peptide.

XX Temporin G; anti-microbial property; anti-fungal property.

XX Rana temporaria.

XX Key Location/Qualifiers

FT Peptide 1..22

FT Protein /note= "Signal peptide"

FT /note= "Mature temporin G peptide; this peptide is claimed under claim 1 on page 20 in the specification"

FT Modified-site 59

FT /note= "C-terminal amide present in the mature peptide"

XX WO9825961-A1.

XX 18-JUN-1998.

XX 12-DEC-1997; 97WO-SE002075.

XX 13-DEC-1996; 96SE-00004593.

XX (SBLV-) SBL VACCIN AB.

XX Barra D, Simmaco M;

XX WPI, 1998-362423/31.

XX N-PSDB; AAV07449.

XX Peptides from the skin of the frog Rana temporaria - useful as anti-microbial or anti-fungal compositions.

XX Claim 1; Page 19, 20; 27pp; English.

XX The present sequence represents the Rana temporaria temporin G anti-microbial peptide encoded by the temporin G cDNA which was isolated from a R. temporaria skin cDNA library. The invention claims for other R. temporaria derived peptides which are claimed to be useful in medicaments for anti-microbial and anti-fungal use

XX SQ Sequence 61 AA;

Query Match 100.0%; Score 306; DB 2; Length 61;
 Best Local Similarity 100.0%; Pred. No. 3.2e-30;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFTLKSLLLPFLGTINSLCEERDADEERDDLEERDVEVEKRPFPVIGRILNGILG 60
 DB 1 MFTLKSLLLPFLGTINSLCEERDADEERDDLEERDVEVEKRPFPVIGRILNGILG 60

QY 61 K 61
 DB 61 K 61

RESULT 2
 AAB18737
 ID AAB18737 standard; protein; 61 AA.
 XX AAB18737;
 DT 22-JAN-2001 (first entry)
 DE A temporin G precursor polypeptide.
 XX Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;
 KW cationic peptide; pathogen resistance.
 XX Rana temporaria.
 OS WO200055337-A1.
 PN WO200055337-A1.
 PD 21-SEP-2000.
 XX 16-MAR-2000; 2000WO-CA000288.
 PF 17-MAR-1999; 99US-0125072P.
 PR (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
 XX Misra S, Kay WD;
 PI WPI; 2000-647077/62.
 DR N-PSDB; AAV75750.
 XX Transgenic plants resistant to broad spectrum of pathogens useful for
 PT producing biologically active cationic peptides, comprises nucleic acid
 PT molecule encoding temporin and/or dermaseptin peptides.
 XX Disclosure; Page 49-50; 58pp; English.
 XX The present sequence represents a temporin precursor polypeptide. The
 CC specification also describes dermaseptin polypeptides. Temporin and
 CC dermaseptin have antibacterial activity. Dermaseptin also inhibits fungal
 CC growth. Cationic peptides derived from temporins and dermaseptins are
 CC used to produce transgenic plants. The transgenic plants are useful for
 CC producing biologically active cationic peptides such as temporins and
 CC dermaseptins in large quantities. The peptide confers broad spectrum
 CC pathogen resistance including enhanced resistance to both fungal and
 CC bacterial pathogens in the transgenic plants. The transgenic plants may
 CC be used in conventional agricultural applications such as food crops,
 CC medical and other applications

XX SQ Sequence 61 AA;

Query Match 100.0%; Score 306; DB 3; Length 61;
 Best Local Similarity 100.0%; Pred. No. 3.2e-30;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFTLKSLLLPFLGTINSLCEERDADEERDDLEERDVEVEKRPFPVIGRILNGILG 60
 DB 1 MFTLKSLLLPFLGTINSLCEERDADEERDDLEERDVEVEKRPFPVIGRILNGILG 60

QY 61 K 61
 DB 61 K 61

RESULT 3
 AAW51841
 ID AAW51841 standard; protein; 61 AA.
 XX AAW51841;
 AC 26-OCT-1998 (first entry)
 DT Rana temporaria temporin B peptide.
 DE Temporin B; anti-microbial property; anti-fungal property.
 XX Rana temporaria.
 OS Key Location/Qualifiers
 FH Peptide 1..22
 FT /note= "Signal peptide"
 FT Protein 47..59
 FT /note= "Mature temporin B peptide; this peptide is
 FT claimed under claim 1 on page 20 in the specification"
 FT Modified-site 59
 FT /note= "C-terminal amide present in the mature peptide"
 XX WO9825961-A1.
 PN 18-JUN-1998.
 PD 12-DEC-1997; 97WO-SE002075.
 PF 13-DEC-1996; 96SE-00004593.
 PR (SBLV-) SBL VACCIN AB.
 PA Barra D, Simmaco M;
 PI WPI; 1998-362423/31.
 DR N-PSDB; AAV07447.
 XX Peptides from the skin of the frog Rana temporaria - useful as anti-
 PT microbial or anti-fungal compositions.
 XX Claim 1; Page 18, 20; 27pp; English.
 PS The present sequence represents the Rana temporaria temporin B anti-
 CC microbial peptide encoded by the temporin B cDNA which was isolated from
 CC a R. temporaria skin cDNA library. The invention claims for other R.
 CC temporaria derived peptides which are claimed to be useful in medicaments
 CC for anti-microbial and anti-fungal use

XX SQ Sequence 61 AA;

Query Match 80.1%; Score 245; DB 2; Length 61;
 Best Local Similarity 75.4%; Pred. No. 1.1e-22;
 Matches 46; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 MFTLKSLLLPFLGTINSLCEERDADEERDDLEERDVEVEKRPFPVIGRILNGILG 60
 DB 1 MFTLKSLLLPFLGTINSLCEERDADEERDDLEERDVEVEKRPFPVIGRILNGILG 60

QY 61 K 61
 DB 61 K 61

RESULT 4
 AAW51842
 ID AAW51842 standard; protein; 58 AA.

XX	OS	Phyllomedusa bicolor.
XX	XX	WO200055337-A1.
PN	XX	
XX	PX	21-SEP-2000.
PD	XX	
XX	XX	16-MAR-2000; 2000WO-CA000288.
XX	PF	
XX	PR	17-MAR-1999; 99US-0125072P.
XX	PP	
XX	PA	(UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
XX	PI	Misra S, Kay WD;
XX	PI	WPI; 2000-647077/62.
DR	DR	N-PSDB; AA75749.
XX	XX	Transgenic plants resistant to broad spectrum of pathogens useful for producing biologically active cationic peptides, comprises nucleic acid molecule encoding temporin and/or dermaseptin peptides.
PT	PT	Disclosure; Page 47; 58pp; English.
XX	PS	
XX	CC	The present sequence represents a dermaseptin precursor polypeptide. The precursor is processed to produce two mature forms, dermaseptin b (AAB18725) and dermaseptin B (AAB18726). Dermaseptin has antibacterial activity, and inhibits fungal growth. Cationic peptides derived from temporins and dermaseptins are used to produce transgenic plants. The transgenic plants are useful for producing biologically active cationic peptides such as temporins and dermaseptins in large quantities. The peptide confers broad spectrum pathogen resistance including enhanced resistance to both fungal and bacterial pathogens in the transgenic plants. The transgenic plants may be used in conventional agricultural applications such as food crops, medical and other applications
XX	SQ	Sequence 78 AA;
		Query Match 33.7%; Score 103; DB 3; Length 78;
		Best Local Similarity 56.8%; Pred. No. 6e-05;
		Matches 21; Conservative 8; Mismatches 6; Indels 2; Gaps
Qy	1	MFTLKSLLLFLGTINLSCEER--DADERDD 35 : : : : : 1 MDILKKSLVLFLGLVLSLICEEKRENEDEKQDD 37
Dd	1	MDILKKSLVLFLGLVLSLICEEKRENEDEKQDD 37
RESULT 6		
AAG62384		
ID	AAG62384	standard; peptide; 24 AA.
AC	AA62384;	
XX		
DT	30-AUG-2001	(first entry)
XX		
DE		Pro-region of temporin G peptide.
XX		
KW		Transgenic plant; cationic peptide; cecropin-mellitin; CEWA; resistance;
KW		antibacterial; antifungal; antimicrobial; food crop; blight; soft rot;
KW		frog; temporin G.
XX		
OS		Rana temporaria.
XX		
PN	WO200136647-A1.	
XX		
PD	25-MAY-2001.	
XX		
PF	14-JUL-2000; 2000WO-CA000826.	
XX		
PR	12-NOV-1999; 99US-0165249P.	
XX		
PA	(UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.	
XX		

PI Misra S., Kay WD., Osusky M;
 XX WPI; 2001-336007/35.
 XX Transgenic plants useful as food crops are resistant to late blight due
 XX to Phytophthora infestans and/or to soft rot due to Erwinia carotovora.
 XX Disclosure; Page 51; 55pp; English.
 XX The present invention relates to a transgenic plant, which expressed a
 CC cationic peptide of the cecropin-mellitin (CEMA) family or related
 CC peptide. CEMA is an antimicrobial peptide with confers resistance to
 CC fungal and bacterial pathogens. Included in the invention are CEMA-
 CC related fusion peptides in which an N-terminal extension peptide is fused
 CC to the CEMA peptide. A pro-region peptide may be used as a fusion
 CC peptide, which neutralises the cationic nature of the CEMA or CEMA-
 CC related peptide and provides enhanced stability in cellular environments,
 CC or decreases the toxicity of the CEMA or CEMA-related peptide to the host
 CC organism. Transgenic plants of the invention may be used in conventional
 CC agricultural applications, such as food crops. The plants may display
 CC resistance to late blight due to Phytophthora infestans and or to soft
 CC rot due to Erwinia carotovora. The present sequence represents a temporin
 CC G pro region peptide, which can be used to modify the CEMA peptides used
 CC in the invention
 XX Sequence 24 AA;
 SQ
 Query Match 31.0%; Score 95; DB 4; Length 24;
 Best Local Similarity 75.0%; Pred. No. 0.00016;
 Matches 18; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 23 EERADERRRDLERDVEVEKR 46
 DB 1 EEERNAEERDRDEPDRVQVEKR 24
 RESULT 7
 ADR88893
 ID ADR88893 standard; protein; 62 AA.
 AC ADR88893;
 XX 18-NOV-2004 (first entry)
 DT Amino acid sequence of tryptophyllin-1 designated pDt-1.
 DE
 XX tryptophyllin-1; pDt-1; vasodilatory; frog; defensive skin secretion;
 KW vasodilation; ischaemic heart disease; ischaemic disease;
 KW vascular stenosis; occlusion; hypertension; blood-brain barrier;
 KW anti-cancer; angiogenesis; healing; transplant; graft;
 KW spinal cord injury; cardiovascular disease; arterial smooth muscle;
 KW central nervous system disorder; infection; inflammation; cancer; tumour;
 KW Hodgkin's disease; non-Hodgkin's lymphoma; multiple myeloma;
 KW haematopoietic malignancy; glioma; pulmonary hypertension; stroke;
 KW atherosclerosis; asthma; ophthalmologic disease; renal failure;
 KW menstrual disorder; obstetric condition; wound; gastroenteric disease;
 KW anaphylactic shock; endotoxic shock.
 XX Pachymedusa dactinolor.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..20
 FT /note= "signal peptide"
 FT Protein 21..62
 FT /note= "mature protein"
 XX WO2004074312-A2.
 PN
 XX 02-SEP-2004.
 PD
 XX 04-FEB-2004; 2004WO-IB000806.
 PF
 XX 05-FEB-2003; 2003GB-00002621.
 PR

PR 06-JUN-2003; 2003GB-00012990.
 XX (UYUL-) UNIV ULSTER.
 PA (SHAW) SHAW C.
 PA (HIRST) HIRST D.
 PA (CHEN) CHEN T.
 PA (OROU) O'ROURKE M.
 XX Shaw C, Hirst D, Chen T, O'rouke M;
 PI WPI; 2004-642491/62.
 DR N-PSDB; ADR88892.
 XX Isolated tryptophyllin peptide obtained from biologically active analog
 PT of Pachymedusa dactinolor tryptophyllin-1, having vasodilatory activity,
 PT useful for treating conditions of vascular insufficiency e.g., ischemic
 PT heart disease.
 PS Disclosure; SEQ ID NO 18; 55pp; English.
 CC The present sequence represents a full length tryptophyllin-1, derived
 CC from Pachymedusa dactinolor and designated pDt-1. The specification
 CC describes tryptophyllin-1 peptides and pDt-1 analogues which have a
 CC vasodilatory activity. Tryptophyllin-1 peptides are isolated from frog
 CC defensive skin secretions. Tryptophyllin-1 peptides of the invention are
 CC useful for preparing a medicament for treating disorders where
 CC vasodilation is beneficial, such as ischaemic heart disease, ischaemic
 CC disease of other organs or organ systems, vascular stenoses, occlusion to
 CC peripheral vessels, or hypertension, and for increasing the transport of
 CC biologically active compounds across the blood-brain barrier, where the
 CC biologically active compound is an anti-cancer drug. They are useful for
 CC promoting angiogenesis, for treating conditions of vascular
 CC insufficiency, to promote healing at sites of transplantation and
 CC grating, and for treating spinal cord injuries. They are also useful for
 CC treating cardiovascular disease, for increasing vasodilation, for
 CC treating hypertension, for dilating arterial smooth muscle. In
 CC combination with other therapeutic agents, peptides of the invention are
 CC useful for treating disorders in the brain including central nervous
 CC system disorder, bacterial, viral and fungal infections, inflammation and
 CC cancer, tumour, Hodgkin's disease, non-Hodgkin's lymphomas, multiple
 CC myeloma and haematopoietic malignancies. Tryptophyllin-1 peptides of the
 CC invention are also useful in treating glaucoma, pulmonary hypertension,
 CC stroke, atherosclerosis, asthma, ophthalmologic disease, renal failure,
 CC menstrual disorder, obstetric conditions, wound, gastroenteric disease,
 CC anaphylactic or endotoxic shock, etc.
 XX Sequence 62 AA;
 SQ
 Query Match 30.1%; Score 92; DB 8; Length 62;
 Best Local Similarity 44.4%; Pred. No. 0.0011;
 Matches 16; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
 QY 4 LKKSLLLLFFLGITNLSCEERDAEERRDLER 39
 DB 4 LKKSFLVFLGFSISFCDEKQDDDEGNEREK 39
 RESULT 8
 AAG66531
 ID AAG66531 standard; protein; 645 AA.
 XX AAG66531;
 XX 22-OCT-2001 (first entry)
 DT Human interferon-alpha induced polypeptide, ERP-70.
 DE
 XX Human; interferon-alpha induced gene; type I interferon treatment;
 KW chronic viral hepatitis; relapsing remitting multiple sclerosis;
 KW neoplastic disease; ERP-70.
 XX Homo sapiens.
 OS

PN WO200159155-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-GB000578.
 XX 11-FEB-2000; 2000GB-00003203.
 PR 11-FEB-2000; 2000GB-00003204.
 PR 11-FEB-2000; 2000GB-00003205.
 PR 11-FEB-2000; 2000GB-00003206.
 PR 11-FEB-2000; 2000GB-00003207.
 PR 11-FEB-2000; 2000GB-00003208.
 PR 11-FEB-2000; 2000GB-00003210.
 PR 11-FEB-2000; 2000GB-00003212.
 PR 11-FEB-2000; 2000GB-00003213.
 PR 11-FEB-2000; 2000GB-00003215.
 PR 11-FEB-2000; 2000GB-00003216.
 PR 11-FEB-2000; 2000GB-00003219.
 PR 11-FEB-2000; 2000GB-00003220.
 PR 11-FEB-2000; 2000GB-00003221.
 PR 11-FEB-2000; 2000GB-00003222.
 PR 17-FEB-2000; 2000GB-00003768.
 XX (PHAR-) PHARMA PACIFIC PTY LTD.
 PA Meritet J, Dron M, Tovey MG;
 PI WPI; 2001-483570/52.
 XX N-PSDB; AAH76458.
 PT Predicting responsiveness of a patient to treatment with a type I
 PT interferon comprising determining the level of induced proteins after
 PT treatment with a type I interferon.
 XX Claim 1; Page 58-60; 133pp; English.
 PS The invention relates to a method for predicting responsiveness of a
 CC patient to treatment with a type I interferon. The method comprises
 CC determining the level of one or more proteins with a 646, 164, 126, 598,
 CC 98, 177, 761, 361, 941, 657, 817, 429, 473, 399, 285 or 303 amino acid
 CC sequence fully defined in the specification after treatment with a type I
 CC interferon. The method allows a physician to determine whether a patient
 CC suffering from chronic viral hepatitis, neoplastic disease or relapsing
 CC remitting multiple sclerosis will respond favourably to Type I interferon
 CC treatment via oromucosal administration. The present sequence is one of
 CC the polypeptides listed above that may be used in the method
 XX Sequence 645 AA;
 Query Match 23.0%; Score 70.5; DB 4; Length 645;
 Best Local Similarity 28.2%; Pred. No. 6.7;
 Matches 20; Conservative 10; Mismatches 16; Indels 25; Gaps 2;
 QY 5 KKSLLLLFLGTLINLSLCE-----EERDADERRDDLEERDVEVEKRF 48
 Db 4 RKAFLLLLGLVQLLAVAGAGPDESSNRNATEDDEEEEDDEEDDLVKSE-- 61
 QY 49 PVIGRLNGIL 59
 Db 62 -----NGVL 65
 RESULT 9
 ID ADO19794
 XX ADO19794 standard; protein; 645 AA.
 AC ADO19794;
 XX 12-AUG-2004 (first entry)
 DT Human PRO polypeptide #359.
 DE Human; PRO; immune related disorder; systemic lupus erythematosus;
 XX
 KW

KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 XX Homo sapiens.
 OS WO2004043361-A2.
 PN 27-MAY-2004.
 XX 06-NOV-2003; 2003WO-US035268.
 PD 08-NOV-2002; 2002US-0425235P.
 XX (GETH) GENENTECH INC.
 PA Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TD;
 PI WPI; 2004-420067/39.
 DR N-PSDB; ADO19793.
 XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.
 XX Claim 7; SEQ ID NO 718; 1731pp; English.
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.
 XX Sequence 645 AA;
 Query Match 23.0%; Score 70.5; DB 8; Length 645;
 Best Local Similarity 28.2%; Pred. No. 6.7;
 Matches 20; Conservative 10; Mismatches 16; Indels 25; Gaps 2;
 QY 5 KKSLLLLFLGTLINLSLCE-----EERDADERRDDLEERDVEVEKRF 48
 Db 4 RKAFLLLLGLVQLLAVAGAGPDESSNRNATEDDEEEEDDEEDDLVKSE-- 61
 QY 49 PVIGRLNGIL 59
 Db 62 -----NGVL 65
 RESULT 10
 ID ABM80947
 XX ABM80947 standard; protein; 645 AA.
 AC ABM80947;
 XX 18-NOV-2004 (first entry)
 DT Tumour-associated antigenic target (TAT) polypeptide PRO2733, SEQ:2443.
 DE Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 XX Tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW

QY 49 PVIGRILNGIL 59
Db 62 -----NGVL 65

RESULT 12
AAU30243
ID AAU30243 standard; protein; 646 AA.

XX AC AAU30243;
XX DT 18-DEC-2001 (first entry)
XX DE Novel human secreted protein #734.

XX KW Human; vaccination; gene therapy; nutritional supplement;
XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX OS Homo sapiens.
XX PN WO200179449-A2.

XX PD 25-OCT-2001.

XX PF 16-APR-2001; 2001WO-US008656.

XX PR 18-APR-2000; 2000US-00552929.

XX PR 26-JAN-2001; 2001US-00770160.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-611725/70.

XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic
XX PT vaccination, testing and therapy.

XX PS Claim 20; Page 266; 765pp; English.

XX CC The invention relates to novel human secreted polypeptides. The
XX CC polypeptides and antibodies to the polypeptides are useful for
XX CC determining the presence of or predisposition to a disease associated
XX CC with altered levels of polypeptide. The polypeptides are also useful for
XX CC identifying agents (agonists and antagonists) that bind to them. Cells
XX CC expressing the proteins are useful for identifying a therapeutic agent
XX CC for use in treatment of a pathology related to aberrant expression or
XX CC physiological interactions of the polypeptide. Vectors comprising the
XX CC nucleic acids encoding the polypeptides and cells genetically engineered
XX CC to express them are also useful for producing the proteins. The proteins
XX CC are useful in genetic vaccination, testing and therapy, and can be used
XX CC as nutritional supplements. They may be used to increase stem cell
XX CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
XX CC and/or nerve tissue growth or regeneration; immune suppression and/or
XX CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
XX CC AAU29510-AAU3304 represent the amino acid sequences of novel human
XX CC secreted proteins of the invention

XX SQ Sequence 646 AA;

Query Match 23.0%; Score 70.5; DB 4; Length 646;
Best Local Similarity 28.2%; Pred. No. 6.7;
Matches 20; Conservative 10; Mismatches 16; Indels 25; Gaps 2;

QY 5 KKSLLLLFLGTLINSLCE-----EERDADEERDDLEERDVEVEKRPF 48
Db 4 RKAFLLLGLLVQLAVAGAGPDESSNRNATEDDEEEEDDEDDLEVKEE-- 61

QY 49 PVIGRILNGIL 59
Db 62 -----NGVL 65

RESULT 13
AAU30491

XX ID AAU30491 standard; protein; 918 AA.

XX AC AAU30491;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secreted protein #982.

XX KW Human; vaccination; gene therapy; nutritional supplement;
XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX OS Homo sapiens.

XX PN WO200179449-A2.

XX PD 25-OCT-2001.

XX PF 16-APR-2001; 2001WO-US008656.

XX PR 18-APR-2000; 2000US-00552929.

XX PR 26-JAN-2001; 2001US-00770160.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-611725/70.

XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic
XX PT vaccination, testing and therapy.

XX PS Claim 20; Page 300; 765pp; English.

XX CC The invention relates to novel human secreted polypeptides. The
XX CC polypeptides and antibodies to the polypeptides are useful for
XX CC determining the presence of or predisposition to a disease associated
XX CC with altered levels of polypeptide. The polypeptides are also useful for
XX CC identifying agents (agonists and antagonists) that bind to them. Cells
XX CC expressing the proteins are useful for identifying a therapeutic agent
XX CC for use in treatment of a pathology related to aberrant expression or
XX CC physiological interactions of the polypeptide. Vectors comprising the
XX CC nucleic acids encoding the polypeptides and cells genetically engineered
XX CC to express them are also useful for producing the proteins. The proteins
XX CC are useful in genetic vaccination, testing and therapy, and can be used
XX CC as nutritional supplements. They may be used to increase stem cell
XX CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
XX CC and/or nerve tissue growth or regeneration; immune suppression and/or
XX CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
XX CC AAU29510-AAU3304 represent the amino acid sequences of novel human
XX CC secreted proteins of the invention

XX SQ Sequence 918 AA;

Query Match 23.0%; Score 70.5; DB 4; Length 918;
Best Local Similarity 28.2%; Pred. No. 9.9;
Matches 20; Conservative 10; Mismatches 16; Indels 25; Gaps 2;

QY 5 KKSLLLLFLGTLINSLCE-----EERDADEERDDLEERDVEVEKRPF 48
Db 4 RKAFLLLGLLVQLAVAGAGPDESSNRNATEDDEEEEDDEDDLEVKEE-- 61

QY 49 PVIGRILNGIL 59
Db 62 -----NGVL 65

RESULT 14
AUS27442

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 17:57:33 ; Search time 295 Seconds
(without alignments)

6750.067 Million cell updates/sec

Title: US-10-719-623A-15

Perfect score: 329

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
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- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	329	100.0	329	17	US-10-719-623-15
2	45	13.7	443	17	Sequence 15, Appl
3	42.4	12.9	665	13	Sequence 1, Appl1
4	42.4	12.9	665	17	Sequence 185531,
5	40.5	12.3	403	11	Sequence 185531,
6	40.2	12.2	4804	18	Sequence 4267, Ap
7	40	12.2	56153	17	Sequence 30217, A
8	39.4	12.0	894	13	Sequence 520, App
9	39.4	12.0	894	13	Sequence 3788, Ap
10	39.4	12.0	8781	15	Sequence 3788, Ap
11	38.8	11.8	1746	18	Sequence 1659, Ap
					Sequence 116, App

12	38.6	11.7	466	9	US-09-864-761-16328
13	38.6	11.7	2211	17	US-10-424-599-44115
14	38.6	11.7	4756	9	US-09-982-091A-3
15	38.6	11.7	23934	9	US-09-764-860-777
16	38.6	11.7	23934	9	US-09-764-877-2536
17	38.6	11.7	23934	9	US-09-764-877-2544
18	38.6	11.7	23934	10	US-09-764-891-7210
19	38.6	11.7	23934	14	US-10-074-095-777
20	38.6	11.7	23934	17	US-10-212-872-777
21	38.6	11.7	23934	17	US-10-242-515-2536
22	38.6	11.7	23934	17	US-10-242-515-2544
23	38.6	11.7	14950	15	US-10-311-455-1230
24	38	11.6	477	13	US-10-027-632-20397
25	38	11.6	477	17	US-10-027-632-20397
26	38	11.6	765	9	US-09-974-300-8246
27	38	11.6	220860	17	US-10-684-190-3
28	37.4	11.4	815	18	US-10-739-930-545
29	37.4	11.4	640681	9	US-09-790-988-1
30	37	11.2	433	9	US-09-878-178-1348
31	37	11.2	433	13	US-10-046-935-1348
32	37	11.2	433	14	US-10-146-502-1348
33	37	11.2	17738	15	US-10-311-455-1511
34	36.8	11.2	370	17	US-10-424-599-44029
35	36.8	11.2	381	18	US-10-425-115-28644
36	36.8	11.2	1176	14	US-10-156-275-5
37	36.8	11.2	5495	14	US-10-156-275-1
38	36.8	11.2	5495	14	US-10-156-275-2
39	36.8	11.2	10592	14	US-10-156-275-51
40	36.8	11.2	10592	14	US-10-156-275-51
41	36.8	11.2	10592	14	US-10-156-275-52
42	36.8	11.2	10592	14	US-10-156-275-52
43	36.6	11.1	6215	15	US-10-311-455-1164
44	36.4	11.1	598	13	US-10-027-632-218332
45	36.4	11.1	598	13	US-10-027-632-218333

ALIGNMENTS

RESULT 1

- US-10-719-623-15
- Sequence 15, Application US/10719623
- Publication No. US20040073977A1
- GENERAL INFORMATION:
- APPLICANT: Misra and Kay
- TITLE OF INVENTION: Transgenic Plants that are Resistant to a Broad Spectrum of Pathogens
- FILE OF INVENTION: of Pathogens
- FILE REFERENCE: 673243
- CURRENT APPLICATION NUMBER: US/10/719,623
- CURRENT FILING DATE: 2003-11-20
- PRIOR APPLICATION NUMBER: 60/125,072
- PRIOR FILING DATE: 1999-03-17
- PRIOR APPLICATION NUMBER: PCT/CA00/00288
- PRIOR FILING DATE: 2000-03-16
- PRIOR APPLICATION NUMBER: 09/936,885
- PRIOR FILING DATE: 2001-09-17
- NUMBER OF SEQ ID NOS: 41
- SOFTWARE: PatentIn Ver. 2.0
- SEQ ID NO 15
- LENGTH: 329
- TYPE: DNA
- ORGANISM: Rana temporaria
- FEATURE:
- NAME/KEY: CDS
- LOCATION: (53)..(238)
- US-10-719-623-15

Query Match 100.0%; Score 329; DB 17; Length 329;

Best Local Similarity 100.0%; Pred. No. 3.9e-78;

Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 CCCTCCAGCTGTCTACATTCATACCACTGACCCAGCCCAAGATGTTTCAC 60

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RESULT 3
US-10-027-632-185531
; Sequence 185531, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129

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RESULT 4
US-10-027-632-185531
; Sequence 185531, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185531

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; LENGTH: 665
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)...(665)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-185531

Query Match      12.9%; Score 42.4; DB 17; Length 665;
Best Local Similarity 53.7%; Pred. No. 0.46;
Matches 88; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 166 AAGCGATGTTGAAGTGAAGAGCGATTTTCCAGTGTGGAAGGAGTACTCAATGCTAT 225
Db 7 AAGATAATTTTAATTTAAATAATGTTCTTCTAGTGTCTTCCATATCCATAACTAAAT 66

Qy 226 TTTGGGAAATTAACCAAAAAAAGTTAAACCTTTTCGAAATGGAATGGAATCATCTAATG 285
Db 67 TTTATGTAACAATCAACTATATCTTATTTTGAGGAATGAATACATATATATATAT 126

Qy 286 TGGATGCTATTTAGCTAAATGCAATCAATGCTTTATATAAAA 329
Db 127 TGGAGAATATCTTTGTGATTTTACAGAAAATATCTATATATA 170

RESULT 5
US-09-864-408A-4267/c
; Sequence 4267, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR FILING DATE: 2001-05-24
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4267
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-864-408A-4267

Query Match      12.3%; Score 40.6; DB 11; Length 403;
Best Local Similarity 51.4%; Pred. No. 1.1;
Matches 94; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

Qy 144 AAGAAGAGATGATCTCGAAGAAGGGATGTTGAAGTGGAAAAAGCGATTTTTCAGTGA 203
Db 293 ATACAAATGATCAGTAGCAATATCTAGTGGCTCATGTGGAAGCAACTTTTTCAGCTT 234

Qy 204 TTGGAAGGATCACTCAATGCTATTTTGGGAAAAATACCAAAAAAGTTAAACTTTGAAA 263
Db 233 TAGTAAAAATATTTCTAGATTTTGAAGAGATAAAGCAATTAATAATTTAGTATGAAGA 174

Qy 264 TGGAAATGGAAATCATCTAATGGAATGTCATTTAGCTAAATGCACATCAATGCTTA 323
Db 173 CAACAGCTACATGAGCTATAGAAATATGCGATATTTCTCAATGGACATAGATGCTTCA 114

Qy 324 TAA 326
Db 113 TCA 111

RESULT 6
US-10-357-930-30217
; Sequence 30217, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endeghe, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30217
; LENGTH: 4804
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 4776, 4777, 4778, 4779, 4780, 4781, 4782, 4783, 4784, 4785,
; LOCATION: 4786, 4787, 4788, 4789, 4790, 4791, 4792, 4793, 4794, 4795,
; LOCATION: 4796, 4797, 4798, 4799, 4800, 4801, 4802, 4803, 4804
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-30217

Query Match      12.2%; Score 40.2; DB 18; Length 4804;
Best Local Similarity 54.4%; Pred. No. 4.4;
Matches 81; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 120 AGGAAGAGAGATGCCGATGAGGAAGAGAGAGATGATCTCGAAGAAGGATGTTGAAG 179
Db 2074 AGGTAGAGAAAGAAAGAAAGAGAGAACTAGAGGAGAGGAGAGAGAGAGAGAGG 2133

Qy 180 TGGAAAAGCGATTTTTCAGTGTGGAAGGATCTCAATGGTATTTTCGAAAAATAAC 239
Db 2134 AGGAAGAGAGAGAAATCAGGAGACTGCAGAAATCTCTTCTAGTAGGAAGAAATAGAAA 2193

Qy 240 CAAAAAAGTTAAACTTTTGGAAATGGAA 268
Db 2194 CAAAAGATGAAAAAGAAATGGATAAGAA 2222

RESULT 7
US-10-221-714A-520/c
; Sequence 520, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: tumor suppressor genes and oncogenes
; FILE REFERENCE: 5013,1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
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Query Match	12.0%	Score 39.4	DB 13	Length 894
Best Local Similarity	54.5%	Prod. No. 3.3		
Matches	79	Conservative	Mismatches 66	Indels 0
QY	139	TCGAAGAAAGACGAGATGATCTCGAAGAAAGGGATGTTGAAGTGGAAAAGCGAATTTTTTC	198	
ph	347	TCGACGATTTTATCTCGAAGAACCAATTAATTTGGAGACTTTACCAAGAAGACTCTATAGTCTCA	288	

; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1659
; LENGTH: 8781
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1659

Query Match 12.0%; Score 39.4; DB 15; Length 8781;
Best Local Similarity 51.4%; Pred. No. 9.6;
Matches 91; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 126 AGAGAGATCCGATCGAAGAAAGAGAGATGATCTCGAAGAGGAGGATGTTCAAGTGGAAA 185
DB 748 AGTAGATAGAAATATAGAAAATAAATTTTAAATGATGATTAAGATTTTGAATAATA 807
QY 186 AGCGATTTTCCAGTGATGGAAGGATCTCAATGTTATTTGGGAAATAACCAAAAA 245
DB 808 TAGAATTATATAAGTTATTAAATATATATATAGATATTTTGGGAGAGAAAAA 867
QY 246 AAGTTAAACCTTGGAAATGGAATGGAATCATCTTAATGTGGAATGTCATTTAGCT 302
DB 868 AAATTAAGATTTGGAAAAATTTATTGAGGGAATAAATTTAGAAAAATTTTTCGTT 924

RESULT 11

US-10-411-910A-116
; Sequence 116, Application US/10411910A
; Publication No. US20040209256A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
; FILE REFERENCE: H2041203-P
; CURRENT APPLICATION NUMBER: US/10/411.910A
; CURRENT FILING DATE: 2003-04-12
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 116
; LENGTH: 1746
; TYPE: DNA
; ORGANISM: Thermoanaerobacter tengcongensis
US-10-411-910A-116

Query Match 11.8%; Score 38.9; DB 18; Length 1746;
Best Local Similarity 51.8%; Pred. No. 6.6;
Matches 88; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 160 CGAAGAAAGGATGTTCAAGTGGAAGAACGATTTTCCAGTGATGTTGGAAGGATCTCAA 219
DB 1449 CAAGTTAAGCGAGGAGAGTCGATGATCTATTATAGAGTGTGGATGCCAGGTGG 1508
QY 220 TGGTATTTGGGAAATAACCAAAAAAGTTAAACCTTTTGGAAATGGAATGGAATCAT 279
DB 1509 CTGTATAATGGTGGAGGACAGCAATCCCAATCTCTTAACGAGATGGAAGATCAAGAA 1568
QY 280 CTATGTGGAATGTCATTTAGCTTAATGTCATCAATGCTTTATATAAAA 329
DB 1569 ATTAAGGGCAAGGCAATTTACGAGATAGACAAGAACCTCGCTATATAGAA 1618

RESULT 12

US-09-864-761-16328
; Sequence 16328, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16328
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL034452.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.63
US-09-864-761-16328

Query Match 11.7%; Score 38.6; DB 9; Length 466;
Best Local Similarity 52.1%; Pred. No. 4;
Matches 86; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 148 AACGATGATCTCGAAGAAAGGATGTTGAAGTGGAAGAACGATTTTCCAGTGATGG 207
DB 26 AGAGAAATTCGGGTATTAGGAAGTTTATCACAAACTTTATTTTCTCTATAATAGA 85
QY 208 AAGGATCTCAATGGTATTTTGGGAAATAACCAAAAAAGTTTAAAACTTTGGAAATGGA 267
DB 86 AAAAAAATGAATAAGTAACAGTCGAGAAAGTTACCAAGTCAATAAAGGAATGGC 145
QY 268 ATTGGAAATCATCTAATGTGGAATGTCATTTAGCTAAATGCACAT 312
DB 146 ATCTGTGATTTTCTATTATTTAAAAACTTTTCTAGACTCAAGCAAAAT 190

RESULT 13
US-10-424-599-44115

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	329	100.0	329	3	US-09-319-730-18	Sequence 18, Appl
2	329	100.0	329	4	US-09-936-885A-15	Sequence 15, Appl
3	212.8	64.7	323	3	US-09-319-730-14	Sequence 14, Appl
4	203.8	61.9	356	3	US-09-319-730-16	Sequence 16, Appl
5	45	13.7	443	4	US-09-936-885A-1	Sequence 1, Appl
6	40.6	12.3	7218	1	US-08-232-463-14	Sequence 14, Appl
7	40.6	12.3	45983	4	US-09-949-016-17010	Sequence 17010, A
8	40.2	12.2	4756	4	US-09-949-016-4455	Sequence 4455, Ap
9	40	12.2	202111	4	US-09-949-016-13877	Sequence 13877, A
10	39.8	12.1	601	4	US-09-949-016-183626	Sequence 183626,
11	39.2	11.9	1664976	4	US-08-916-421B-1	Sequence 1, Appl
12	39.2	11.9	1664976	4	US-09-692-570-1	Sequence 1, Appl
13	37.8	11.5	5852	1	US-07-867-106-2	Sequence 2, Appl
14	37.4	11.4	640681	4	US-09-790-988-1	Sequence 1, Appl
15	36.8	11.2	1176	1	US-08-602-010A-5	Sequence 5, Appl
16	36.8	11.2	1176	1	US-08-680-726A-5	Sequence 5, Appl
17	36.8	11.2	1176	3	US-09-092-409-5	Sequence 5, Appl
18	36.8	11.2	5495	1	US-08-602-010A-1	Sequence 1, Appl
19	36.8	11.2	5495	1	US-08-602-010A-2	Sequence 2, Appl
20	36.8	11.2	5495	1	US-08-680-726A-1	Sequence 1, Appl
21	36.8	11.2	5495	1	US-08-680-726A-2	Sequence 2, Appl
22	36.8	11.2	5495	3	US-09-092-409-1	Sequence 1, Appl
23	36.8	11.2	5495	3	US-09-092-409-2	Sequence 2, Appl
24	36.8	11.2	10592	1	US-08-680-726A-51	Sequence 51, Appl
25	36.8	11.2	10592	1	US-08-680-726A-51	Sequence 51, Appl
26	36.8	11.2	10592	1	US-08-680-726A-52	Sequence 52, Appl
27	36.8	11.2	10592	1	US-08-680-726A-52	Sequence 52, Appl

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us-10-719-623a-15.rn1

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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17010
; LENGTH: 45983
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(45983)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17010

Query Match      12.3%; Score 40.6; DB 4; Length 45983;
Best Local Similarity 51.4%; Pred. No. 0.72; Indels 0; Gaps 0;
Matches 94; Conservative 0; Mismatches 89;

QY 144 AAGAAGAGATGATCTCGAAGAAAGGATGTTGAAGTGAAGAAAGCGATTTTTCAGTGA 203
DB 34909 ATACAAATGATCAGTAGCAATATCTAGTGGCTCATGTGAAGCAACTTTTTTCTCAGCTT 34850
QY 204 TTGGAAGGATACCTCAATGTTATTTTGGGAAATAACCAAAAAGTTTAAACTTTTGGAAA 263
DB 34849 TAGTAAAAATATTCTAGATTTTGGGAAGATGAAGCAATTAATAATAGTAGTAGAGA 34790
QY 264 TGGAAATGGAATCATCTAATGTGGAATGTCATTTAGCTAAATGCACATCAAAATGCTTTA 323
DB 34789 CAAACAGCTACATGAGCTATAGAAATATGCGATATTTCTCAATGGACATAGATGCTTCA 34730
QY 324 TAA 326
DB 34729 TCA 34727

RESULT 8
US-09-949-016-4455
; Sequence 4455, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4455
; LENGTH: 4756
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
US-09-949-016-4455

Query Match      12.2%; Score 40.2; DB 4; Length 4756;
Best Local Similarity 54.4%; Pred. No. 0.43; Indels 0; Gaps 0;
Matches 81; Conservative 0; Mismatches 68;

QY 120 AGAAGAGAGATGCGGATGAAGAAAGAGATGATCTCGAAGAAAGGATGTTGAAG 179
DB 2030 AGGTAGAGAAGAAAGAAAGAGGAGAACTAGAGAAAGAGGAGGAGGAGG 2089
QY 180 TCGAAAGCGATTTTTCAGTGAAGGATGATCTCAATGTTATTTTGGGAAATAAC 239
DB 2090 AGGAAGAAAGAAATCAGGAGACTGCAGATTCCTCTTAGTAGAAGAAATAGAAA 2149
QY 240 CAAAAAAGTTAAACTTTGGAAATGGA 268
DB 2150 CAAAAGATGAAGAAAGAAATGGATAAGAA 2178

; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13877
; LENGTH: 202111
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(202111)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13877

Query Match      12.2%; Score 40; DB 4; Length 202111;
Best Local Similarity 53.9%; Pred. No. 1.7; Indels 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 70;

QY 119 GAGGAAGAGAGATGCGGATGAAGAAAGAGATGATCTCGAAGAAAGGATGTTGAA 178
DB 154940 GAGGAAGATGAATTTGGAGACGTAGACAGAGAAAGCAACATGTTGGGCTTTGGGA 154881
QY 179 GTCGAAAAGCGATTTTTCAGTGAAGGATGATCTCAATGTTATTTTGGGAAATAA 238
DB 154880 GCTGAGAGGAGATTTATTTCTTAAACATAGTAAGAGCCATCAGAGGGTTTAAAGCAAGAA 154821
QY 239 CCAAAAAAGCTTAAACTTTTGGAAATGGAATT 270
DB 154820 CATAAAATAATTTGTACATTATTAAGGCATTT 154789

RESULT 10
US-09-949-016-183626
; Sequence 183626, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183626
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
US-09-949-016-183626

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Query Match          12.1%; Score 39.8; DB 4; Length 601;
Best Local Similarity 51.4%; Pred. No. 0.27; Indels 0; Gaps 0;
Matches 92; Conservative 0; Mismatches 87;

QY 148 AAGAGATCTCGAAGAAAGGATGTTGAAGTGGAAAAGCGATTTTTCAGTGTATGG 207
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 AAATGATCAGTAGCAATATCTAGTGGCTCATGTGAAGCAACTTTTTTCTCAGCTTTAGT 60

QY 208 AAGGATCTCAATGCTATTTTGGGAAATACCAAAAAGTTAAACTTTGGAATGGA 267
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AAAAATATTTCTAGATTTTGAAGAAGATAAAGCAATTAATAATTAGTATGAAGACAAA 120

QY 268 ATTGAAATCATCTAATGTGAATGCTATTAGCTAAATGCACATCAAAATGCTTTATAA 326
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 CAGCTACATGAGCTATAGAAATATGGCATATTTCTCAATGACATAGAAATGCTTCATCA 179

RESULT 11
US-08-916-421B-1/c
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98159)..(98159)
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; LOCATION: (231980)..(231980)
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; NAME/KEY: misc feature
; LOCATION: (234187)..(234187)
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; LOCATION: (234220)..(234220)
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; LOCATION: (234814)..(234814)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309398)..(309398)
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; NAME/KEY: misc feature
; LOCATION: (309418)..(309418)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (312837)..(312837)
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (319226)..(319226)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559167)..(559167)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
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; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (682442)..(682442)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (713652)..(713652)
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; NAME/KEY: misc feature
; LOCATION: (741684)..(741684)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779455)..(779455)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779676)..(779676)
; OTHER INFORMATION: n equals a, t, c, or g

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us-10-719-623a-15.rni

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NAME/KEY: misc feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (1349491)..(1349491)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (1470091)..(1470091)
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LOCATION: (1569020)..(1569020)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1664854)..(1664854)
OTHER INFORMATION: n equals a, t, c, or g
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US-08-916-421B-1

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Query Match 11.9%; Score 39.2; DB 4; Length 1664976;
Best Local Similarity 50.5%; Pred. No. 5.8;
Matches 95; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 141 AGAAGAGAGATGATCTCGAAGAAAGGATGTTGAAGTGAAAGCGATTTTCCAG 200
DB 1641889 AAGACCTTAAGATTTCTTTGAAATAATGATAAGACATTTGAAGATACTTTTGATG 1641830

QY 201 TGATTTGGAAGGATCTCAATGGTATTTTCGGAATAATAACCAAAAGTTAAACTTTGG 260
DB 1641829 AATTTTAAAGATAATTTAGGAATAATAAGACATATATCTGAAAGATTTGAAATAGTCA 1641770

QY 261 AATGAATTTGGAATCTATCTATGTGGATGCTATTAGCTAAATGCACATCAATGTC 320
DB 1641769 AAAAGAGCTTAAAAATAATGAAATAATAAGAAATTATTGCAATTATTACCTTAAAGAAA 1641710

QY 321 TTATATAA 328
DB 1641709 TTAGAGAA 1641702
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RESULT 12
US-09-692-570-1/c

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Sequence 1, Application US/09692570
Patent No. 6797466
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
Patent No. 6797466
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275C1
CURRENT APPLICATION NUMBER: US/09/692,570
CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
PRIOR APPLICATION NUMBER: US 08/916,421
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
NAME/KEY: misc feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
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Best Local Similarity 50.5%; Pred. No. 5.8;

Matches 95; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

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Qy 141 AAGAAGAGAGATGATCTCGAAGAGAGGATGTTGAAGTGGAAAGCGATTTTTCAG 200
Db 1641889 AAGACCTTAAAGATTTCTTTGAAAAAATGGATAAGACATTTGTAAGATAACTTTTGATG 1641830
Qy 201 TGATTGGAAGGATCACTCAATGGTATTTTGGAAAAATAACCAAAAAAGTTAAAACTTTGG 260
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Qy 261 AAATGGAATTGGAAATCATCTAATGTGGAATGTCATTTAGCTAAATGCACATCAAAATGTC 320
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Qy 321 TTATATAA 328
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Db 1641709 TTAGAGAA 1641702

RESULT 13
US-07-867-106-2
; Sequence 2, Application US/07867106
; Patent No. 5389526
; GENERAL INFORMATION:
; APPLICANT: Slade, Martin B
; APPLICANT: Chang, Andy C M
; APPLICANT: Williams, Keith L
; TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
; TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/867,106
; FILING DATE: 19920625
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PJ 7187
; APPLICATION NUMBER: PCT/AU90/00530
; FILING DATE: 02-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Feeney, Joanne Longo
; REGISTRATION NUMBER: 35,134
; REFERENCE/DOCKET NUMBER: RICE-0002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5852 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2378..5038
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; NAME/KEY: CDS
; LOCATION: 2378..5038
; US-07-867-106-2

Query Match 11.5%; Score 37.8; DB 1; Length 5852;
Best Local Similarity 52.2%; Pred. No. 2.1; 77; Indels 0; Gaps 0;
Matches 84; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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QY 182 GAAAGCGATTTTCCATGATTTGAAGGATCTCAATGGTATTTTGGGAAATAACCA 241
Db 5015 GAAGATGAAGAGCAGATGGTATTTGAATTCATCTTTAAATAATTAATAATA 5074
QY 242 AAAAGATTAAACCTTTGGAATTTGGAATTTGGAATTCATCTA 282
Db 5075 AAAAAAAGAAATGATTTCAATTTAAATATATACATATATA 5115

RESULT 14
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEKI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT FILING DATE: 2001-02-23
; CURRENT APPLICATION NUMBER: US/09/790,988
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
; US-09-790-988-1

Query Match 11.4%; Score 37.4; DB 4; Length 640681;
Best Local Similarity 51.5%; Pred. No. 13;
Matches 86; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

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QY 185 AAGCGATTTTTCAGTGTGGAAGGATCTCAATGGTATTTTGGGAAAAATAACCAAA 244
Db 279416 AAAAAATTTAATTCATTTTAGAAAAATACAACTAAGAAATCTGAAGAAAAATAATAGAA 279475
QY 245 AAAGTTAAACCTTTGGAATTTGGAATTTGGAATTCATCTAATTTGGAAT 291
Db 279476 AAAGAGAAATAGTTGGAAGAAATAGTAAATACATAATAGATT 279522

RESULT 15
US-08-602-010A-5/c
; Sequence 5, Application US/08602010A
; Patent No. 5753235
; GENERAL INFORMATION:
; APPLICANT: Haanes, Elizabeth J.
; APPLICANT: Frank, Rexann S.
; TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,010A
; FILING DATE: February 15, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-46
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 5:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1176 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
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; LOCATION: 1..1176
; US-08-602-010A-5

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Query Match      11.2%; Score 36.8; DB 1; Length 1176;
Best Local Similarity 58.0%; Pred. No. 2.2;
Matches 65; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Db      781 TCCAAATATCATTTCTCTGAGGATAATGAGATGCAGAGCATCAAGAAGAGAGATGAGGAGG 722

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Db      721 AGGAGGATGAAGATGAGGATATAGAGGACATCTTGGAGAGCTTCAAGTT 670

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Search completed: March 31, 2005, 18:26:04
Job time : 105 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 14:45:33 ; Search time 1389 Seconds
(without alignments)
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Title: US-10-719-623A-15
Perfect score: 329
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Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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6: gb_pat.*
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8: gb_pl.*
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11: gb_sts.*
12: gb_sv.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	329	100.0	329	5	RTTEMPORG
2	329	100.0	329	6	ARI176040
3	329	100.0	329	6	BD268889
4	329	100.0	329	6	BD063212
5	217.8	66.2	347	5	S69903
6	212.8	64.7	323	5	RTTEMPORB
7	212.8	64.7	323	6	ARI176038
8	212.8	64.7	323	6	BD063210
9	203.8	61.9	356	5	RTTEMPORH
10	203.8	61.9	356	6	ARI176039
11	203.8	61.9	356	6	BD063211
12	195.8	59.5	363	5	REBRE1E
13	165.4	50.3	318	5	RRU22393
14	149.6	45.5	294	5	AJ427746
15	125.4	38.1	362	5	RP1414584
16	120	36.5	317	5	RP1427747
17	119.8	36.4	310	5	AJ583866
18	104	31.6	384	5	RESCC1B
19	101.2	30.8	339	5	RT251567

20	98.8	30.0	338	5	REBRE2EP	X77832 R.esculenta
21	93.2	28.3	1111	5	OSC544062	AJ544062 Odorrana
22	92	28.0	417	5	RP1427748	AJ247748 Rana pipi
23	90.2	27.4	355	5	RRU22392	U22392 Rana rugosa
24	86	26.1	317	5	RT251566	AJ251566 Rana temp
25	71.8	21.8	6188	5	AF213015	AF213015 Rana rugo
26	57.8	17.6	316	5	AV218784	AV218784 Phyllomed
27	55.4	16.8	393	5	KSE318759	AJ318759 Kassina s
28	53.2	16.2	310	5	PSA549500	AJ549500 Phyllomed
29	51.2	15.6	327	5	PSA564792	AJ564792 Phyllomed
30	51.2	15.6	358	5	PSA564791	AJ564791 Phyllomed
C	31	48.4	14.7	200600	2	AC131324 Mus muscu
32	47.4	14.4	354	5	PBI251876	AJ251876 Phyllomed
33	47	14.3	351	5	AAAJ5188	AJ005188 agalychni
34	46.8	14.2	341	5	PDA507318	AJ507318 Pachymedu
C	35	46.6	14.2	165861	10	AC122791 Mus muscu
36	46.4	14.1	358	5	PSA564794	AJ564794 Phyllomed
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38	45.2	13.7	333	5	PBY16566	Y16566 Phyllomedus
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C	43	44.8	13.6	237541	2	AC112564 Rattus no
44	44.4	13.5	345	5	AV218780	AY218780 Litoria c
45	44.4	13.5	351	5	AV218779	AY218779 Litoria c

ALIGNMENTS

RESULT 1
RTTEMPORG 329 bp mRNA linear VRT 02-OCT-2003
LOCUS R.temporaria mRNA for temporin G precursor.
DEFINITION Y09395
ACCESSION Y09395
VERSION Y09395.1 GI:1771591
KEYWORDS temporin G.
SOURCE Rana temporaria (common frog)
ORGANISM Rana temporaria
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana; Rana.
REFERENCE 1 Simmaco, M., Mignogna, G., Canofeni, S., Miele, R., Mangoni, M.L. and Barra, D.
AUTHORS Temporins, antimicrobial peptides from the European red frog Rana temporaria
TITLE Eur. J. Biochem. 242 (3), 788-792 (1996)
JOURNAL MEDLINE 97175050
PUBMED 9022710
REFERENCE 2 (bases 1 to 329)
AUTHORS Barra, D.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1996) D. Barra, Universita La Sapienza, Dipartimento Di Scienze Biochimiche, Piazzale Aldo Moro 5, 00185 Roma, ITALY
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source Location/Qualifiers
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/function="antibacterial activity"
/codon_start=1
/evidence=experimental
/product="temporin G precursor"
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/evidence=experimental

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Best Local Similarity 100.0%; Pred. No. 1.6e-65;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTCCAGCTGTCTACATCTCATTAACCAACTGAACACCCGAGCCCAAGAGTTTCAC 60
DB 1 CCCCTCCAGCTGTCTACATCTCATTAACCAACTGAACACCCGAGCCCAAGAGTTTCAC 60
QY 61 CTTGAAGAAATCCCTCTTACTCTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 120
DB 61 CTTGAAGAAATCCCTCTTACTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 120
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DB 121 GGAAGAGAGAGATGCCGATCGAAGAAAGAGAGATGATCTCGAAGAAAGGAGTTTGAAGT 180
QY 181 GGAAGAGAGATTTTCCAGTGTGTTTCCAGTGTGTTTCCAGTGTGTTTCCAGTGTGTT 240
DB 181 GGAAGAGAGATTTTCCAGTGTGTTTCCAGTGTGTTTCCAGTGTGTTTCCAGTGTGTT 240
QY 241 AAAAAAGTTAAACCTTTCGAAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG 300
DB 241 AAAAAAGTTAAACCTTTCGAAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG 300

RESULT 2
AR176040
LOCUS AR176040 329 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 18 from patent US 6310176.
ACCESSION AR176040
VERSION AR176040.1 GI:17917339
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Barra, D. and Simmaco, M.
TITLE Antimicrobially active polypeptides
JOURNAL Patent: US 6310176-A 18 30-OCT-2001;
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Best Local Similarity 100.0%; Pred. No. 1.6e-65;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GGAAGAGAGAGATGCCGATCGAAGAAAGAGAGATGATCTCGAAGAAAGGAGTTTGAAGT 180
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DB 121 GGAAGAGAGATGCCGATCGAAGAAAGAGAGATGATCTCGAAGAAAGGAGTTTGAAGT 180
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QY 301 CTAATGACATCAAAATGCTTTATAAAAA 329
DB 301 CTAATGACATCAAAATGCTTTATAAAAA 329

BD268889 329 bp DNA linear PAT 17-JUL-2003
Transgenic plant having tolerance to wide-area pathogen.
BD268889
BD268889.1 GI:33078657
JP 2002538828-A/2.
Rana temporaria (common frog)
SOURCE Rana temporaria
ORGANISM Rana
Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana;
Rana.
REFERENCE
AUTHORS Misra, S. and Kay, W.W.
TITLE Transgenic plant having tolerance to wide-area pathogen
JOURNAL Patent: JP 2002538828-A 2 19-NOV-2002;
UNIVERSITY OF VICTORIA INNOVATION AND DEVELOPMENT CORP
COMMENT OS Rana temporaria (european common frog)
PN JP 2002538828-A/2
PD 19-NOV-2002
PF 16-MAR-2000 JP 2000605754
PR 17-MAR-1999 US 60/125072
PI SANTOSH MISRA, WILLIAM W KAY
PC A01H5/00,C07K14/415/C12N5/10,C12N15/09,C12N15/00,C12N5/00 CC
Transgenic plant having tolerance to wide-area pathogen PH Key
Location/Qualifiers
(53)..(235).
FT CDS Location/Qualifiers
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/mol_type="genomic DNA"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.6e-65;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTCCAGCTGTCTACATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 60
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QY 121 GGAAGAGAGATGCCGATCGAAGAAAGAGAGATGATCTCGAAGAAAGGAGTTTGAAGT 180
DB 121 GGAAGAGAGATGCCGATCGAAGAAAGAGAGATGATCTCGAAGAAAGGAGTTTGAAGT 180
QY 181 GGAAGAGAGATTTTCCAGTGTGTTTCCAGTGTGTTTCCAGTGTGTTTCCAGTGTGTT 240
DB 181 GGAAGAGAGATTTTCCAGTGTGTTTCCAGTGTGTTTCCAGTGTGTTTCCAGTGTGTT 240
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QY 301 CTAATGCGACATCAAAATGCTTTATATAAA 329
Db 301 CTAATGCGACATCAAAATGCTTTATATAAA 329

RESULT 4
BD063212
LOCUS DEFINITION Antimicrobially active polypeptides. linear PAT 27-AUG-2002
ACCESSION BD063212
VERSION BD063212.1 GI:22608815
KEYWORDS JP 2001506495-A/3.
SOURCE Rana temporaria (common frog)
ORGANISM Rana temporaria

REFERENCE 1 (bases 1 to 329)
AUTHORS Barra, D. and Simmaco, M.
TITLE Antimicrobially active polypeptides
JOURNAL Patent: JP 2001506495-A 3 22-MAY-2001;
COMMENT SBL VACCIN AB
OS Rana temporaria
PN JP 2001506495-A/3
PD 22-MAY-2001 JP 1998526559
PF 12-DEC-1997 JP 1998526559
PR 13-DEC-1996 SE 9604593-5
PI DONNATELLA BARRA, MAURIZIO SIMMACO
PC C07K14/46, C07K7/08, A61K33/56
CC cDNA clone Rt-17
FH Key Location/Qualifiers
FT CDS (53)..(238)
FT mat peptide (191)..(229)
FT polyA signal (323)..(327)..
FEATURES
Source
1..329
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ORIGIN
Query Match 100.0%; Score 329; DB 6; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.6e-65;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTCCAGCTGTCTACATTTCTCATACCAACTGAACCCGAGCCCAAGATGTTTAC 60
Db 1 CCCCTCCAGCTGTCTACATTTCTCATACCAACTGAACCCGAGCCCAAGATGTTTAC 60

QY 61 CTTGAAGAAATCCCTCTTACTCTCTTTCTCTTGGGACATCAACTTATCTCTGTGA 120
Db 61 CTTGAAGAAATCCCTCTTACTCTTTCTCTTGGGACATCAACTTATCTCTGTGA 120

QY 121 GGAAGAGAGATGCCGATGAAGAGAGAGATGATCTCGAAGAGAGATGTTGAAGT 180
Db 121 GGAAGAGAGATGCCGATGAAGAGAGAGATGATCTCGAAGAGAGATGTTGAAGT 180

QY 181 GGAAGAGAGATGTTTCCAGTGATGGAAGGATCTCAATGGTATTTTGGGAAATTAACC 240
Db 181 GGAAGAGAGATGTTTCCAGTGATGGAAGGATCTCAATGGTATTTTGGGAAATTAACC 240

QY 241 AAAAAAGTTAAACCTTTGGAAATGGAATGGAATCATCTAATGGAATGTCATTAG 300
Db 241 AAAAAAGTTAAACCTTTGGAAATGGAATGGAATCATCTAATGGAATGTCATTAG 300

QY 301 CTAATGCGACATCAAAATGCTTTATATAAA 329
Db 301 CTAATGCGACATCAAAATGCTTTATATAAA 329

RESULT 5
S69903
LOCUS DEFINITION Ranalexin=antimicrobial peptide polypeptide [Rana
catesbeiana-bullfrogs, metamorphic tadpoles, skin cells, mRNA, 347
nt].
ACCESSION S69903
VERSION S69903.1 GI:546211
KEYWORDS Rana catesbeiana (bullfrog)
SOURCE Rana catesbeiana
ORGANISM Rana catesbeiana
REFERENCE 1 (bases 1 to 347)
AUTHORS Clark, D.P., Durell, S., Maloy, W.L. and Zasloff, M.
TITLE Ranalexin. A novel antimicrobial peptide from bullfrog (Rana
catesbeiana) skin, structurally related to the bacterial
antibiotic, polymyxin
JOURNAL J. Biol. Chem. 269 (14), 10849-10855 (1994)
MEDLINE 94193792
PUBMED 8144672
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsg 146812] from the original journal article.
FEATURES
Location/Qualifiers
1..347
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/mol_type="mRNA"
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Method: conceptual translation with partial peptide
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/db_xref="GI:546212"
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KRFGLGLIKIVPAMICAVTKK"

ORIGIN
Query Match 66.2%; Score 217.8; DB 5; Length 347;
Best Local Similarity 84.8%; Pred. No. 6.4e-40;
Matches 279; Conservative 0; Mismatches 47; Indels 3; Gaps 3;

QY 3 CCTCCAGCTGTCTACATTTCTCATACCAACTGAACCCGAGCCCAAGATGTTTACCT 62
Db 3 CTTCCAGCTGTCTACATTTCTCATACCAACTGAACCCGAGCCCAAGATGTTTACCT 61

QY 63 TGAAGAAATCCCTCTTACTCTCTTTCTCTTGGGACATCAACTTATCTCTGTGAGG 122
Db 62 TGAAGAAATCCCTCTTACTCTCTTTCTCTTGGGACATCAACTTATCTCTGTGAGG 121

QY 123 AAGAGAGATGCCGATGAAGAGAGATGATCTCGAAGAGAGATGTTGAAGTGG 182
Db 122 AAGAGAGAAATCCCGAAGAGAGAGATGATCTCGAAGAGAGATGTTGAAGTGG 181

QY 183 AAAAGCGATTTTTCAGTGATGGAAGGATCTCAATGGTAT-TTTGGGAAATTAACCA 241
Db 182 AAAAGCGATTTTGGGAGGCTTAATAAGATCGTTCAGCAATGATTTGTGAGTACCA 241

QY 242 AAAAAAGTTAAACCTTTGGAAA-TGGAAATTGGAATCATCTAATGGAATGTCATTAG 300
Db 242 AAAAAAGTTGAAACTTTGGAACTTTGAAATCATCTGATGTGAGATATCATTTAG 301

QY 301 CTAATGCGACATCAAAATGCTTTATATAAA 329
Db 302 CTAATATCACACCATGCTTTATATAAA 330

RESULT 6
RTTEMPORB

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LOCUS RTTEMPORB 323 bp mRNA linear VRT 02-OCT-2003
 DEFINITION R.temporaria mRNA for temporin B precursor.
 ACCESSION Y09393
 VERSION Y09393.1 GI:1771589
 KEYWORDS temporin B.
 SOURCE Rana temporaria (common frog)
 ORGANISM Rana temporaria
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana;
 Rana.
 REFERENCE 1
 AUTHORS Simmaco,M., Mignogna,G., Canofeni,S., Miele,R., Mangoni,M.L. and Barra,D.
 TITLE Temporins, antimicrobial peptides from the European red frog Rana temporaria
 JOURNAL Eur. J. Biochem. 242 (3), 788-792 (1996)
 MEDLINE 97175050
 PUBMED 9022710
 REFERENCE 2 (bases 1 to 323)
 AUTHORS Barra,D.
 TITLE Direct Submission
 JOURNAL Submitted (11-NOV-1996) D. Barra, Universita La Sapienza, Dipartimento Di Scienze Biochimiche, Piazzale Aldo Moro 5, 00185 Roma, ITALY
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 /clone_lib="RT-5"
 37..222
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 /evidence=experimental
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 /db_xref="GOA:P79874"
 /db_xref="UniProt/Swiss-Prot:P79874"
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 /note="amidated C-terminus; post-translational modification"
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 Best Local Similarity 83.4%; Pred. No. 9.1e-39;
 Matches 257; Conservative 0; Mismatches 42; Indels 9; Gaps 1;
 QY 22 TCATACCACTGAACCCGAGCCCAAGAGTTCACCTTGAGAGAGAGATGCCGATGA 81
 DB 6 TCTGAGCCAACTGAACCCGAGCCCAAGAGTTCACCTTGAGAGAGAGATGCCGATGA 65
 QY 82 CCTTTTCTCTGGGACCACATCACTTATCTCTGTGAGAGAGAGATGCCGATGA 141
 DB 66 CCTCTTTTCTCTGGGACCACATCACTTATCTCTGTGAGAGAGAGATGCCGATGA 125
 QY 142 AGAAGAAGAGATGATCTCGAAGAAAGGATGTTGAAGTGGAAAAACGATTTTCCAGT 201
 DB 126 AGAAGAAGAGATGAACACAGATGAAAGGGATGTTCAAGTGGAAAAACGATTTTACCAAT 185
 QY 202 GATTGGAAGGATCACTCAATGTTTGGAAAAATAACCAAAAGTTAAACTTTGGA 261
 DB 186 TGTGGAACCTGCTCAAGAGCTTGTGGAAAAATAACCA-----AAATGTTAAG 236
 QY 262 AATGGAATTGGAATCATCTAATGTGGAATGTCATTTAGCTAAATGCACATCAATGTCT 321
 DB 237 AATGGAATTGGAATCATCTGATGTGGAATATCAITTTAGCTAAATGCACATCAATGTCT 296
 QY 322 TATAAAAA 329
 DB 297 TATTTAAA 304
 RESULT 8
 LOCUS BD063210
 DEFINITION Antimicrobially active polypeptides.
 ACCESSION BD063210
 VERSION BD063210.1 GI:22608813
 KEYWORDS JP 2001506495-A/1.
 SOURCE Rana temporaria (common frog)
 ORGANISM Rana temporaria
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana;
 Rana.
 REFERENCE 1 (bases 1 to 323)
 AUTHORS Barra,D. and Simmaco,M.
 TITLE Antimicrobially active polypeptides
 JOURNAL Patent: JP 2001506495-A 1 22-MAY-2001;

Db 237 AATGGAATTGGAATCATCTGATGTGGAATCATTTAGCTAAATGCACAGATGTCT 296
 QY 322 TATAAAAA 329
 DB 297 TATTTAAA 304
 RESULT 7
 LOCUS ARL176038
 DEFINITION Sequence 14 from patent US 6310176.
 ACCESSION ARL176038
 VERSION ARL176038.1 GI:17917337
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 323)
 AUTHORS Barra,D. and Simmaco,M.
 TITLE Antimicrobially active polypeptides
 JOURNAL Patent: US 6310176-A 14 30-OCT-2001;
 FEATURES Location/Qualifiers
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 Query Match 64.7%; Score 212.8; DB 6; Length 323;
 Best Local Similarity 83.4%; Pred. No. 9.1e-39;
 Matches 257; Conservative 0; Mismatches 42; Indels 9; Gaps 1;
 QY 22 TCATACCACTGAACCCGAGCCCAAGAGTTCACCTTGAGAGAGATGCCGATGA 81
 DB 6 TCTGAGCCAACTGAACCCGAGCCCAAGAGTTCACCTTGAGAGAGAGATGCCGATGA 65
 QY 82 CCTTTTCTCTGGGACCACATCACTTATCTCTGTGAGAGAGAGATGCCGATGA 141
 DB 66 CCTCTTTTCTCTGGGACCACATCACTTATCTCTGTGAGAGAGAGATGCCGATGA 125
 QY 142 AGAAGAAGAGATGATCTCGAAGAAAGGATGTTGAAGTGGAAAAACGATTTTCCAGT 201
 DB 126 AGAAGAAGAGATGAACACAGATGAAAGGGATGTTCAAGTGGAAAAACGATTTTACCAAT 185
 QY 202 GATTGGAAGGATCACTCAATGTTTGGAAAAATAACCAAAAGTTAAACTTTGGA 261
 DB 186 TGTGGAACCTGCTCAAGAGCTTGTGGAAAAATAACCA-----AAATGTTAAG 236
 QY 262 AATGGAATTGGAATCATCTAATGTGGAATGTCATTTAGCTAAATGCACATCAATGTCT 321
 DB 237 AATGGAATTGGAATCATCTGATGTGGAATATCAITTTAGCTAAATGCACAGATGTCT 296
 QY 322 TATAAAAA 329
 DB 297 TATTTAAA 304
 RESULT 8
 LOCUS BD063210
 DEFINITION Antimicrobially active polypeptides.
 ACCESSION BD063210
 VERSION BD063210.1 GI:22608813
 KEYWORDS JP 2001506495-A/1.
 SOURCE Rana temporaria (common frog)
 ORGANISM Rana temporaria
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana;
 Rana.
 REFERENCE 1 (bases 1 to 323)
 AUTHORS Barra,D. and Simmaco,M.
 TITLE Antimicrobially active polypeptides
 JOURNAL Patent: JP 2001506495-A 1 22-MAY-2001;

Dipartimento Di Scienze Biochimiche, Piazzale Aldo Moro 5, 00185
Roma, ITALY

Location/Qualifiers

1. .356

/organism="Rana temporaria"

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79. .255

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/evidence=experimental

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79. .144

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217. .252

/product="temporin H"

/note="amidated C-terminus; post-translational
modification"

/evidence=experimental

peptide

peptide

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Similarity 61.9%; Score 203.8; DB 5; Length 356;
%67; Conservative 0; Mismatches 42; Indels 18; Gaps 2;

3 CCTCCAGCTGCTACATTCATACCACCACTGAACACCGAGGCCAACAAAGATGTTCACT 62
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
19 CTTCAGCGGCTCATATTCGTAGCACCACTGAATACCCGAGCCAAAGATGTTCACT 88
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
13 TGAAGAATCCCTCTTACTCCTTTCTCTTGCGACCACTCAACTTATCTCTGTGAGG 122
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
19 TGAAGAATCCCTGTTACTCCTCTTTCTCTTGCGACCACTCAACTTATCTCTGTGAGG 148
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
13 AAGAGAGAGATCCGATGAAGAAAGAGATGATCTCGAAGAAAGGGATGTTGAAGTGG 182
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
19 AAGAGAGAAATGCAGAAAGAAAGAGATGAACACAGATGAAGAGGGATGTTCAAGTGG 208
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
13 AAACCGATTCTTCCAGTGATGGAAGATACTCAATGGTATTTTTGGGAAAATAACCA 242
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
19 AAAACGACTTTCACC-----AAACCTGCTCAAGAGCTTGTGGGAAAATAACCA - 258
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
13 AAAAAGTTAAAACTTTGGAATGGAATGGAATCATCTTAATGTGGAATGTCATTTAGCT 302
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
19 -----AAATGTTAAGATGGAATGGAATCATCTGATGTGGAATATCATTTAGCT 310
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
13 AAATGCACATCAAAATGCTTATAAAA 329
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 AAATGCGCAACAGATGCTTATTTAAA 337
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AR176039 356 bp DNA linear PAT 17-DEC-2001

Sequence 16 from patent US 6310176.

AR176039

AR176039.1 GI:17917338

. Unknown.
Unknown.
Unclassified.
1 (bases 1 to 356)
Barra,D. and Simmaco,M.
Antimicrobially active polypeptides
Patent: US 6310176-A 16 30-OCT-2001;
Location/Qualifiers

source	1. .356	
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ORIGIN		
Query Match	61.9%; Score 203.8; DB 6; Length 356;	
Best Local Similarity	81.7%; Pred. No. 1.1e-36;	
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QY	3	CTCCAGCTGTCTACATTCTCATTAACCAACTGAACCAACCCGAGCCCAAGAGATGTTTCACTT 62
DB	29	CTTCAGCGCTCTACATTCTGAGCAACCACTGAACCAACCCGAGCCCAAGAGATGTTTCACTT 88
QY	63	TGAAGAAATCCCTTTACTTCTCTTTCTTCTTGGGACCACTCAACTTATCTCTCTGTGAGG 122
DB	89	TGAAGAAATCCCTTTACTTCTCTTTCTTCTTGGGACCACTCAACTTATCTCTCTGTGAGG 148
QY	123	AAGAGAGATGCCGATGAAGAAAGAGATGATCTCGAAGAAAGGATGTTGAAGTGG 182
DB	149	AAGAGAGAAATGCAGAAGAAAGAGAGATGAACCAAGATGAAGAGGATGTTCAAGTGG 208
QY	183	AAAACGCGATTTTTCAGTGTGGAAGGATCACTCAATGGTATTTTGGGAAATTAACCAA 242
DB	209	AAAACGACTTTCAC-----AAACCTGCTCAAGAGCTTGTGGGAAATTAACCA- 258
QY	243	AAAAAGTTAAACTTTTGGAAATGGAATGGAATCATCTAATGTGAATGTCATTTAGCT 302
DB	259	-----AAAATGTTAAGATGGAATGGAATCATCTGATGTGAATATCATTTAGCT 310
QY	303	AAATGCACATCAATGCTTTATAAAAA 329
DB	311	AAATGCGCAACAGATGCTTTATTAAA 337
RESULT 12		
REBRE1E		
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DEFINITION	R.esculenta mRNA for brevinin-1E.	
ACCESSION	X77831	
VERSION	X77831.1 GI:488372	
KEYWORDS	brevinin.	
SOURCE	Rana esculenta (edible frog)	
ORGANISM	Rana esculenta	
REFERENCE	1	
AUTHORS	Simmaco, M., Mignogna, G., Barra, D. and Bossa, F.	
TITLE	Antimicrobial peptides from skin secretions of Rana esculenta.	
JOURNAL	Molecular cloning of cDNAs encoding esculentin and brevinins and isolation of new active peptides	
MEDLINE	J. Biol. Chem. 269 (16), 11956-11961 (1994)	
PUBMED	94216303	
AUTHORS	2 (bases 1 to 363)	
TITLE	Simmaco, M.	
JOURNAL	Direct Submission	
FEATURES	Submitted (10-FEB-1994) M. Simmaco, Nodo Nazionale Italiano (area di, ricerca CNR-Bari), Via Amendola 168/5, 70126 Bari, ITALY	
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source	1. .356	
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Query Match	61.9%; Score 203.8; DB 6; Length 356;	
Best Local Similarity	81.7%; Pred. No. 1.1e-36;	
Matches 267; Conservative	0; Mismatches 42; Indels 18; Gaps 2;	
QY	3	CTCCAGCTGTCTACATTCTCATTAACCAACTGAACCAACCCGAGCCCAAGAGATGTTTCACTT 62
DB	29	CTTCAGCGCTCTACATTCTGAGCAACCACTGAACCAACCCGAGCCCAAGAGATGTTTCACTT 88
QY	63	TGAAGAAATCCCTTTACTTCTCTTTCTTCTTGGGACCACTCAACTTATCTCTCTGTGAGG 122
DB	89	TGAAGAAATCCCTTTACTTCTCTTTCTTCTTGGGACCACTCAACTTATCTCTCTGTGAGG 148
QY	123	AAGAGAGATGCCGATGAAGAAAGAGATGATCTCGAAGAAAGGATGTTGAAGTGG 182
DB	149	AAGAGAGAAATGCAGAAGAAAGAGAGATGAACCAAGATGAAGAGGATGTTCAAGTGG 208
QY	183	AAAACGCGATTTTTCAGTGTGGAAGGATCACTCAATGGTATTTTGGGAAATTAACCAA 242
DB	209	AAAACGACTTTCAC-----AAACCTGCTCAAGAGCTTGTGGGAAATTAACCA- 258
QY	243	AAAAAGTTAAACTTTGGAATGGAATGGAATCATCTAATGTGAATGTCATTTAGCT 302
DB	259	-----AAAATGTTAAGATGGAATGGAATCATCTGATGTGAATATCATTTAGCT 310
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RESULT 11		
BD063211		
LOCUS	356 bp	DNA linear PAT 27-AUG-2002
DEFINITION	Antimicrobially active polypeptides.	
ACCESSION	BD063211	
VERSION	BD063211.1 GI:22608814	
KEYWORDS	JP 2001506495-A/2.	
SOURCE	Rana temporaria (common frog)	
ORGANISM	Rana temporaria	
REFERENCE	1 (bases 1 to 356)	
AUTHORS	Barra, D. and Simmaco, M.	
TITLE	Antimicrobially active polypeptides	
JOURNAL	Patent: JP 2001506495-A 2 22-MAY-2001;	
COMMENT	SBL VACCIN AB	
	OS Rana temporaria	
	PN JP 2001506495-A/2	
	PD 22-MAY-2001	
	PF 12-DEC-1997 JP 1998526559	
	PR 13-DEC-1996 SE 9604593-5	
	PI DONATELLA BARRA, MAURIZIO SIMMACO	
	PC C07K14/46, C07K7/08, A61K33/56	
	CC cDNA clone Rt-6	
	FH Key	
	FT CDS	
	FT mat peptide	
	FT polyA signal	
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Query Match	61.9%; Score 203.8; DB 6; Length 356;	
Best Local Similarity	81.7%; Pred. No. 1.1e-36;	
Matches 267; Conservative	0; Mismatches 42; Indels 18; Gaps 2;	

	Best Local Similarity	80.1%; Pred. No. 7.5e-35;	Matches	270; Conservative	0; Mismatches	57; Indels	10; Gaps	3;
Qy	3	CCTCCAGCTGTCATTTCTCATAAACCAACTGAACCACCGCAGGCCCAAAGATGTTCACCT	62					
Db	7	CTTCCAGCTATCTATATTCTCCGCACCAACTGAACCATCTGAGTCCAAAGATGTTCACCT	66					
Qy	63	TGAAGAAATCCCTCTTACTCTTTTTCTTCTCTGGACCATCAACTTATCTCTGTGAGG	122					
Db	67	TGAAGAATCCAATGTTACTCTTTTCTCTTGGACCATCAACTTATCTCTGTGAGG	126					
Qy	123	AAGAGAGAGATGCCGAT---GAAGAAAAGAAGAGATGATCTCGAAGAAGGGATGTTGAAG	179					
Db	127	AAGAGAGAGATGCCGATGAAGAAGAAAAGAAGACAATCCAGATGAAGTGAAGTTGAG	186					
Qy	180	TGGAAGAAGCGATTTTTTCCAGTGATTTGGAAGGATACTCAATGGTAGTTTGGGAAAA---	235					
Db	187	TGGAAAAACGATTTCTTCCATTTGTGGCAGCTCTGGCTGCTAAATTTCTTGCCGAAAAATAT	246					
Qy	236	TAACCAAAAAAAGTTAAACCTTTGGAAA---TGGAATTGGNAATCATCTAATGTGGGAATG	292					
Db	247	TTTGTAANAATAAACCAAAAAATGTTTGAACCTTTGGAAATGGAAATCATCTGATGTGGAAAA	306					
Qy	293	TCAATTTAGCTAAATGCACATCABAATGCTTTATAAAA	329					
Db	307	TCATTTAGCTAAATAACACATCAGATGCTTTATAAAA	343					

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                        /translations="MTFLKKSLLLFLGLTISLCEERNADDEEKRDVEVEKRFIG
ALPKVASKVLPSVFCAITKCC"
     mat_peptide       158..229
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ORIGIN
Query Match          50.3%; Score 165.4; DB 5; Length 318;

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Matches -232; Conservative		0;	Mismatches 61;	Indels 10; Gaps 2;
Qy	27	ACCAACTGACCAACCCGAGCCCAAGATGTTACCTTGAAGAAATCCCTCTTACTCCTTT	86	
Db	9	ACCAACTGAACTACCAAGAACCCCAAGATGTTACCTTGAAGAAATCCCTCTTACTCCTTT	68	
Qy	87	TC TTCCTTGGGACCATCACTTATCTCTCTGTGAGGAAGAGAGAGATGCCGATGAAGAA	146	
Db	69	TC TTCCTTGGGACCATCAGCTTATCTCTGTGAGGAAGAGAGAAATGCCGATGAAGAG	128	
Qy	147	GAAGAGATGATCTCGAAGAAAGGGATGTTGAAGTGGAAAAGCGATTTTTTCCAGTGATTG	206	
Db	129	AAAAAGAGATGTTGAAG--TGAAAACGATTTTTTGGGAGCACTCTTCAAGGTGGCTTC	186	
Qy	207	GAAGGATCTCAATGGTATTTTGGGAAAAATAACAAAAAAGTTTAAACCTTTGGAAATGG	266	
Db	187	TAAGGTCTGCCATCAGTTTTTTTGTGCAATTACCAAAAAATGTTTAAACCTT-----A	238	
Qy	267	AATTGGAAATCATCTTAATGTGGAAATGTCATTTTAGCTTAAATGCATCAATGCTTATATA	326	
Db	239	AATTGGAAATCATCTGATTTGGAATATCATTCAGCTAAATGCATCAGATGCTTATATA	298	
Qy	327	AAA 329		
Db	299	AAA 301		

RESULT	14
LOCUS	RP1427746
DEFINITION	Rana pipiens mRNA for brevinnin 1pb.
ACCESSION	AJ427746
VERSION	AJ427746.1 GI:20145828
KEYWORDS	antimicrobial peptide; brevinnin 1pb.
SOURCE	Rana pipiens (northern leopard frog)
ORGANISM	Rana pipiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;
REFERENCE	Pantherana. 1
AUTHORS	Chen, T., Farragher, S., Bjourson, A.J., Orr, D.F., Rao, P. and Shaw, C.
TITLE	Granular gland transcriptomes in stimulated amphibian skin secretions
JOURNAL	J. Biochem. 371, 125-130 (2003)
REFERENCE	2 (bases 1 to 294)
AUTHORS	Farragher, S.M.
TITLE	Direct Submission
JOURNAL	Submitted (10-JAN-2002) Farragher S.M., School of Biomedical Sciences, University of Ulster, Cromore Road, N. Ireland., UNITED KINGDOM

FEATURES
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 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:8404"
 /tissue_type="skin"
 /dev_stage="adult"
 /country="USA"
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 /db_xref="GI:20145929"
 /db_xref="GOA:Q8QFQ5"
 /db_xref="UniProt/Swiss-Prot:Q8QFQ5"
 /translation="WFTLNKFLLLFFLGLTINLSFCEENASEERIDBPDDETVVEVK
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 4..63
 139. .210
 sig_peptide
 mat_peptide
 evidence=experimental

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 14:38:32 ; Search time 256 Seconds
(without alignments)
7607.793 Million cell updates/sec

Title: US-10-719-623a-15

Perfect score: 329

Sequence: 1 cccctccagctgtctacatt.....catcaaatgtcttataaaaa 329

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseqn1980b:*
- 3: Geneseqn2000a:*
- 4: Geneseqn2000b:*
- 5: Geneseqn2001a:*
- 6: Geneseqn2001b:*
- 7: Geneseqn2002a:*
- 8: Geneseqn2002b:*
- 9: Geneseqn2003a:*
- 10: Geneseqn2003b:*
- 11: Geneseqn2003cs:*
- 12: Geneseqn2004a:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	100.0	329	2	Aav07449 Rana temp
2	329	100.0	329	3	Aaa75750 cDNA enco
3	212.8	64.7	323	2	Aav07447 Rana temp
4	203.8	61.9	336	2	Aav07448 Rana temp
5	46.8	14.2	341	13	ADR8892 Nucleotid
6	45	13.7	443	3	Aaa75749 cDNA enco
7	40.6	12.3	403	6	Abn77187 Human ORF
8	40.2	12.2	414	10	Adc30694 Human nov
9	40.2	12.2	4804	5	Abv30199 Human pro
10	40	12.2	56153	4	Aas46794 Tumour su
11	39.4	12.0	8781	6	Ab133686 Human imm
12	39.2	11.9	64976	2	AAV21209 16
13	38.6	11.7	466	4	AAI36639 Probe: #53
14	38.6	11.7	4755	6	ABK52611
15	38.6	11.7	23934	4	AAK71442
16	38.6	11.7	23934	4	AAAL36171
17	38.6	11.7	23934	4	AAAL36179
18	38.6	11.7	23934	4	AAAL04522
19	38.6	11.7	23934	4	AAAS28343
20	38.6	11.7	23934	4	ABL97446 Human tes

21	38.6	11.7	23934	5	ABAL9145	Human ner
22	38.6	11.7	23934	8	ABX59167	CDNA enco
23	38.6	11.7	23934	8	ABX59159	CDNA enco
24	38.6	11.7	23934	10	ADG41539	Human res
25	38.6	11.7	23934	11	ADI97313	Human res
26	38.6	11.7	23934	12	ADJ29917	Human mus
27	38.6	11.7	23934	12	ADJ29909	Human mus
28	38.4	11.7	14950	6	ABL33257	Human imm
29	38	11.6	765	6	ABK80955	Bacillus
30	38	11.6	220860	12	ADN36595	Human pro
31	37.8	11.5	5852	2	AAQ11710	Dictyoste
32	37.8	11.5	177866	10	ADL13935	Osteoarth
33	37.4	11.4	747	3	AAC38796	Arabidops
34	37.4	11.4	110000	6	ABA92787 2	Continuat
35	37	11.2	300	5	AAS8181	DNA enco
36	37	11.2	436	6	ABL37759	Human col
37	37	11.2	3502	4	ABL07145	Drosophil
38	37	11.2	8152	4	ABL07144	Drosophil
39	37	11.2	17738	6	ABL33538	Human imm
40	36.8	11.2	402	5	AA575450	DNA enco
41	36.8	11.2	600	2	AAV86185	EST clone
42	36.8	11.2	1176	2	AAV66903	Canine he
43	36.8	11.2	1176	4	AAE26723	Canine he
44	36.8	11.2	5495	2	AAAT75590	Canine he
45	36.8	11.2	5495	2	AAV66900	Canine he

ALIGNMENTS

RESULT 1
AAV07449
ID AAV07449 standard; cDNA; 329 BP.
XX
AC AAV07449;
XX
XX
DT 26-OCT-1998 (first entry)
XX
DE Rana temporaria temporin G cDNA.
XX
KW Temporin G; anti-microbial property; anti-fungal property; ss.
XX
OS Rana temporaria.
XX
FH Key Location/Qualifiers
CDS 53..238
FT /tag= a
FT /product= "Temporin G peptide"
FT sig_peptide 53..118
FT /tag= b
FT mat_peptide 191..229
FT /tag= c
FT polyA_signal 323..327
FT /tag= d
XX
WO9825961-A1.
XX
PN 18-JUN-1998.
XX
PD 12-DEC-1997; 97WO-SE002075.
XX
PR 13-DEC-1996; 96SE-00004593.
XX
PA (SBLV-) SBL VACCIN AB.
XX
PI Barra.D, Simmaco M;
XX
DR WPI; 1998-362423/31.
DR P-PSDB; AAW51843.
XX
PT Peptides from the skin of the frog Rana temporaria - useful as anti-microbial or anti-fungal compositions.


```

FT XX                               /*tag= d
PN WO9825961-A1.
XX 18-JUN-1998.
XX 12-DEC-1997; 97WO-SE002075.
XX 13-DEC-1996; 96SE-00004593.
XX (SBLV-) SBL VACCIN AB.
XX Barra D, Simmaco M;
XX WPI; 1998-362423/31.
XX P-PSDB; AAW51841.
XX Peptides from the skin of the frog Rana temporaria - useful as anti-
PT microbial or anti-fungal compositions.
XX Claim 11; Page 18; 27pp; English.
XX The present sequence represents the Rana temporaria temporin B cDNA
CC isolated from a R. temporaria skin cDNA library. The cDNA encodes a
CC temporin B peptide which has anti-microbial properties. The invention
CC claims for other R. temporaria derived peptides which are claimed to be
CC useful in medicaments for anti-microbial and anti-fungal use
XX
XX Sequence 323 BP; 119 A; 57 C; 64 G; 83 T; 0 U; 0 Other;

Query Match 64.7%; Score 212.8; DB 2; Length 323;
Best Local Similarity 83.4%; Pred. No. 2.6e-48;
Matches 257; Conservative 0; Mismatches 42; Indels 9; Gaps 1;

QY 22 TCATAACCAACTGAACCAACCGAGCCCAAGAGTGTTCACCTTCAAGAAATCCCTCTTACT 81
DB 6 TCTGAGCCCACTGAACCAACCGAGCCCAAGAGTGTTCACCTTGAAGAAATCCCTGTACT 65
QY 82 CTTTTTCTCTTGGGACCATCAACTTATCTCTGTGAGGAAGAGAGATCCCGATGA 141
DB 66 CTTCTTTTCTTGGGACCATCAACTTATCTCTGTGAGGAAGAGAGAAATGCAGAAGA 125
QY 142 AGAAGAAGAGATGATCTCAAGTGTGTAAGTGTGGAAGAAAGCGATTTTTCAGT 201
DB 126 AGAAGAAGAGATGATGATCAAGTGTGTAAGTGTGGAAGAAAGCGATTTTTCAGT 185
QY 202 GATTGGAAGGATCTCAAGTGTGTAAGTGTGGAAGAAAGCGATTTTTCAGT 261
DB 186 TGTGGAAGGATCTCAAGTGTGTAAGTGTGGAAGAAAGCGATTTTTCAGT 236
QY 262 AATGGAATGGAATCATCTAATGTGGAATGTCAATTTAGCTAATGCACATCAAAATGTCT 321
DB 237 AATGGAATGGAATCATCTAATGTGGAATGTCAATTTAGCTAATGCACATCAAAATGTCT 296
QY 322 TATAAAA 329
DB 297 TATTTAAA 304

RESULT 4
AAV07448
ID AAV07448 standard; cDNA; 356 BP.
XX
XX AAV07448;
XX
XX 26-OCT-1998 (first entry)
XX
XX Rana temporaria temporin H cDNA.
XX
XX Temporin H; anti-microbial property; anti-fungal property; ss.
XX
XX Rana temporaria.

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FH Key Location/Qualifiers
FT CDS 79..255
FT sig_peptide /product= "Temporin H peptide"
FT mat_peptide /tag= b
FT polyA_signal /tag= c
FT /tag= d
XX WO9825961-A1.
XX 18-JUN-1998.
XX 12-DEC-1997; 97WO-SE002075.
XX 13-DEC-1996; 96SE-00004593.
XX (SBLV-) SBL VACCIN AB.
XX Barra D, Simmaco M;
XX WPI; 1998-362423/31.
XX P-PSDB; AAW51842.
XX Peptides from the skin of the frog Rana temporaria - useful as anti-
PT microbial or anti-fungal compositions.
XX Claim 11; Page 18; 27pp; English.
XX The present sequence represents the Rana temporaria temporin H cDNA
CC isolated from a R. temporaria skin cDNA library. The cDNA encodes a
CC temporin H peptide which has anti-microbial properties. The invention
CC claims for other R. temporaria derived peptides which are claimed to be
CC useful in medicaments for anti-microbial and anti-fungal use
XX
XX Sequence 356 BP; 124 A; 69 C; 72 G; 91 T; 0 U; 0 Other;

Query Match 61.9%; Score 203.8; DB 2; Length 356;
Best Local Similarity 81.7%; Pred. No. 7.8e-46;
Matches 267; Conservative 0; Mismatches 42; Indels 18; Gaps 2;

QY 3 CTCCAGCTGTCTACATTTCTATCAACCAACTGAACCAACCGAGCCCAAGAGATGTTCACT 62
DB 29 CTTCCAGCGTCTACATTTCTGAGCACCACCACTGAACCTACCGAGCCCAAGAGATGTTCACT 88
QY 63 TGAAGAAATCCCTCTTACTCTCTTCTTCTTGGGACCATCAACTTATCTCTCTGTGAGG 122
DB 89 TGAAGAAATCCCTCTTACTCTCTTCTTCTTGGGACCATCAACTTATCTCTCTGTGAGG 148
QY 123 AAGAGAGAGATCCGATGAAGAAAGAGAGATGATCTCGAAGAAAGCGGATGTTGAAGTGG 182
DB 149 AAGAGAGAAATCGAGAGAAAGAAAGAGAGATGAACAGATGAAGAGGATGTTCAAGTGG 208
QY 183 AAAAGCGATTTTTCAGTGTGGAAGGATCACTCAATGATTTTGGGAAAATAACCA 242
DB 209 AAAAGCGATTTTCACC-----AAACCTGCTCAAGAGCTTGTGTTGGGAAAATAACCA- 258
QY 243 AAAAGTTTAAACTTTGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG 302
DB 259 -----AAAATGTTAAGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG 310
QY 303 AAATGCACATCAATGCTTTTATAAAA 329
DB 311 AAATGCACACAGATGCTTTTATAAAA 337

RESULT 5
ADR88892
ID ADR88892 standard; cDNA; 341 BP.
XX
XX ADR88892;

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Query Match	12.2%;	Score 40;	DB 4;	Length 56153;	Matches 91;	Conservative 0;	Mismatches 86;	Indels 0;	Gaps 0;
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QY 126 AGAGAGATCCGATGAAGAAAGAGATGATCTCGAAGAAAGGATGTTGAAGTCGAAA 185
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
748 AGTTAGATAGAAATAGAAAAATAAATTTTAAATAATCAATAAGATTTTGAAAAATA 807
QY 186 AGCGATTTTTCAGTATGGAAGGATCTCAATGTTATTTTGGGAAAAATACCAAAAA 245
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
808 TAGAATTATATAAAGTTATTAAATATATAATATATATAGATATTTTTCAGGGAGAGAAAA 867
QY 246 AAGTTAAACTTTGGAATGGAATGGAATCACTAAATGCGAATGTCATTTAGCT 302
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
868 AAATTAAAGTTTGGAAATTTTATTTCAGGGAATAATTTTAGGAAAAATTTTTCGGTT 924

RESULT 12
AAV21209_16/c
Continuation (17 of 17) of AAV21209 from base 1600001 (Methanococcus jannaschii circular
WP Sequence split into 17 fragments LOCUS AAV21209 Accession Aav21209
WP Fragment Name Begin End
WP AAV21209_00 1 110000
WP AAV21209_01 100001 210000
WP AAV21209_02 200001 310000
WP AAV21209_03 300001 410000
WP AAV21209_04 400001 510000
WP AAV21209_05 500001 610000
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WP AAV21209_07 700001 810000
WP AAV21209_08 800001 910000
WP AAV21209_09 900001 1010000
WP AAV21209_10 1000001 1110000
WP AAV21209_11 1100001 1210000
WP AAV21209_12 1200001 1310000
WP AAV21209_13 1300001 1410000
WP AAV21209_14 1400001 1510000
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Query Match 11.98; Score 39.2; DB 2; Length 64976;
Best Local Similarity 50.5%; Pred. No. 7.4;
Matches 95; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 141 AAGAAAGAGAGATGATCTCGAAGAAAGGATGTTGAAGTGGAAAAAGCGATTTTTCAG 200
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
41889 AAGACCTTAAAGATTTCTTTGAAAAATGGAATAAGACATTTGTAAGATAACTTTTGATG 41830
QY 201 TGAATGGAAGGATCACTCAATGGTATTTTGGGAAAAATACCAAAAAAGTTAAACITTTGG 260
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41829 AATTTTAAAGATAATTGAGGAATATAAAGACATAATATCTGAAAAAGTTGAAATAGTCA 41770
QY 261 AAATGGAATTGGAATCATCTAATGTGGAATGTCATTTAGCTAAATGCACATCAAAATGTC 320
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
41769 AAAAAGAAAGTTAAAAATGAATAATGAATAATTAAGAAATTTATTTGAAATTTTACCTAAAGAAA 41710
QY 321 TTATAAAA 328
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
41709 TTAGAGAA 41702

RESULT 13
AAI36639
ID AAI36639 standard; DNA; 466 BP.
XX AC AAI36639;
XX
XX 17-OCT-2001 (first entry)
XX DE
XX DE Probe #5325 used to measure gene expression in human placenta sample.
XX KW
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX OS genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200157272-A2.

QY 148 AAGAGATGATCTCGAAGAAAGGATGTTGAAGTGGAAAAAGCGATTTTTCAGTATGG 207
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
26 AAGAGAAATTCGGCTATTAGGAAGTTTATCACAAGACTTATTTTCTCTATATAGA 85
QY 208 AAGGATCACTCAATGGTATTTTGGGAAAAATACCAAAAAAGTTAAACCTTTGGAATGGA 267
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
86 AAAAAAATCAATAGGTAACAGTCAGAGAAAGTTACCAAGTCAAAATAAAGGAATGGC 145
QY 268 ATTGGAATCATCTAATGTGGAATGTCATTTAGCTAAATGCACAT 312
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
146 ATCTGTGATTTTCTATTATTTAAAAACTTTTCTAGACTCAAGCAAAAT 190

RESULT 14
ABK52611
ID ABK52611 standard; DNA; 4755 BP.
XX AC ABK52611;
XX
XX 27-AUG-2002 (first entry)
XX DE
XX DE DNA encoding human Claspin protein.
XX KW
XX KW Chk1 protein; SQ/TQ motif; isoelectric point; cell cycle progression; ds;
XX KW nuclear localisation signal; DNA replication checkpoint; benign neoplasm;
XX KW cell proliferative disorder; malignant neoplasm; human; claspin; gene.
XX OS Homo sapiens.
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XX FH 1. .331
XX misc_feature /tag= a
XX FT /note= "Specifically claimed in claim 9"
XX FT CDS 81. .4079
XX FT /tag= b
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XX FT misc_feature 799. .903
XX PN
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XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR,
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX
XX Claim 25; SEQ ID NO 5325; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP).
XX The present sequence is one such probe. The probes are useful for
XX producing a microarray for predicting, measuring and displaying gene
XX expression in samples derived from human placenta. The probes are useful
XX for antenatal diagnosis of human genetic disorders
XX
XX Sequence 466 BP; 172 A; 64 C; 64 G; 166 T; 0 U; 0 Other;
XX
Query Match 11.7%; Score 38.6; DB 4; Length 466;
Best Local Similarity 52.1%; Pred. No. 1.8;
Matches 86; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 148 AAGAGATGATCTCGAAGAAAGGATGTTGAAGTGGAAAAAGCGATTTTTCAGTATGG 207
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26 AAGAGAAATTCGGCTATTAGGAAGTTTATCACAAGACTTATTTTCTCTATATAGA 85
QY 208 AAGGATCACTCAATGGTATTTTGGGAAAAATACCAAAAAAGTTAAACCTTTGGAATGGA 267
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
86 AAAAAAATCAATAGGTAACAGTCAGAGAAAGTTACCAAGTCAAAATAAAGGAATGGC 145
QY 268 ATTGGAATCATCTAATGTGGAATGTCATTTAGCTAAATGCACAT 312
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
146 ATCTGTGATTTTCTATTATTTAAAAACTTTTCTAGACTCAAGCAAAAT 190

RESULT 14
ABK52611
ID ABK52611 standard; DNA; 4755 BP.
XX AC ABK52611;
XX
XX 27-AUG-2002 (first entry)
XX DE
XX DE DNA encoding human Claspin protein.
XX KW
XX KW Chk1 protein; SQ/TQ motif; isoelectric point; cell cycle progression; ds;
XX KW nuclear localisation signal; DNA replication checkpoint; benign neoplasm;
XX KW cell proliferative disorder; malignant neoplasm; human; claspin; gene.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 1. .331
XX misc_feature /tag= a
XX FT /note= "Specifically claimed in claim 9"
XX FT CDS 81. .4079
XX FT /tag= b
XX FT /product= "Human Claspin protein"
XX FT misc_feature 799. .903
XX PN
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FT FT /*tag= c
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FT misc_feature 1232. 1543
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FT misc_feature 2964. 4756
FT /*tag= f
FT /note= "Specifically claimed in claim 9"

XX WO200233115-A2.

XX 25-APR-2002.

XX 17-OCT-2001; 2001WO-US032316.

XX 17-OCT-2000; 2000US-0241246P.

XX (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX Kumagai A, Dunphy WG;

XX WPI; 2002-454610/48.

XX P-PSDB; AAU97587.

XX Novel Claspin polypeptide specifically interacting with chk1 protein
FT useful for identifying compound that modulates cell cycle progression and
FT for treating cell proliferative disorder like neoplasm.

XX Claim 7; Fig 2; 97pp; English.

CC The present invention relates to a new substantially pure Claspin
CC polypeptide that specifically interacts with a Chk1 protein, having SQ/TQ
CC motifs, an isoelectric point of 4.5 and at least one nuclear localisation
CC signal. The method of the invention is useful for identifying a compound
CC that modulates cell cycle progression and for modulating cell cycle
CC progression in a cell. The invention is useful for the proper operation
CC of DNA replication checkpoint in the cell cycle. The method is also
CC useful for treating a disorder associated with cell cycle progression
CC e.g. cell proliferative disorder such as benign or malignant neoplasm.
CC The molecules of the invention are also useful for detecting the altered
CC levels of claspin expression. The present nucleic acid sequence encodes
CC the human Claspin protein of the invention

XX SQ Sequence 4755 BP; 1626 A; 896 C; 1227 G; 1006 T; 0 U; 0 Other;

Query Match 11.7%; Score 38.6; DB 6; Length 4755;
Best Local Similarity 53.7%; Pred. No. 4.1;
Matches 80; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 120 AGGAAGAGAGATGCCGATGAAGAAGAGAGATCTCGAAGAAAGGAGTGTGAAG 179
Db 2026 AGGTAGAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2085
QY 180 TGGAAGAGCGATTTTTCGATGATTTGGAAGGATCTCAATGCTATTTGGGAAATAAC 239
Db 2086 AGGAAGAAAGAAAGAAATCAGGAGACTGCAGAAATTCCTTCTAGTAGTGAAGAAATAGAAA 2145
QY 240 CAAAAAGCTTAAACTTTTGGAAATGGA 268
Db 2146 CAAAAGATGAAAAAGAAATGGATAAGAA 2174

RESULT 15

AAK71442/c

ID AAK71442 standard; DNA; 23934 BP.

XX AC AAK71442;

XX DT 06-NOV-2001 (first entry)

XX

DE XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26254.
KW XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytotatic; gene therapy; vaccine; metastasis; ds.
OS XX Homo sapiens.
PN XX WO200157182-A2.
XX 09-AUG-2001.
XX 17-JAN-2001; 2001WO-US001354.
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
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XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483426/52.
DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Disclosure; SEQ ID NO 26254; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the cell to express the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent
CC diagnosis and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 23934 BP; 7023 A; 4365 C; 4761 G; 7785 T; 0 U; 0 Other;
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QY 176 GAAAGTGGAAAAAGCGATTTTTTCCAGTGATTGGAGGATACCTCAATGGTATTTTGGGAAA 235
DB 4447 CAAAAGTAAAGAGATAAAATTCCTCATGATGAAGTCTCTGAAGTCATCTTTAAGTTAAT 4388
QY 236 TAACCAAAAAAGCTTAAACTTTGGAATGGAATTCATCAATCTGGAATGTC 295
DB 4387 GGTATAAAAAATTAATAATTTTCTAAGTTCAATAAAAAATCAAGTCATTGAGTAAGTAC 4328
QY 296 TTTTAG 300
DB 4327 TATTG 4323

Search completed: March 31, 2005, 17:34:10
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